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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
                                                                                                                                                                  Result
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                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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AAY94001
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348.847 Million cell updates/sec
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BCMA protein
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 RESULT 1
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AAW/5/83	AAE09244	AAR29814		AAW57891	AAR98351	AAU09900	AAY23925	AAW48374	AAW64568	AAW61196	AA014136	AAE15492	AAE22243	ABB81483	AAE22242	AAE22270	AAE22268	AAE22271	AAE22269	AAE15487	AAE22267	26	AAE22244	ABB81489	AAE15489	AAE15486	AAE15485	AAE15488	AAB60699	AAE00507	AAE15491	AAE15501	E15	AAY71980
Human lymphocyte s	TACI splice	S receptor kinase	Human related adhe	Human PYK-2 protei	Probin tyrosine ki			Mouse related adhe	Murine protein tyr	eir		-murine	Human JST576 (BAFF	Human Ztnfr12 prot	matur		BAFF	Human BAFF recepto	BAFF re	B-cel	BAFF	Human BAFF recepto	മ		BCMA-hu	B-cell		-			-murine	B cell	B cell m	Murine B cell matu

ALIGNMENTS

Key Domain WPI; 2000-558405/51. BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock. Seed B, Ting A; 24-FEB-1999; 24-FEB-2000; 2000WO-US04925 31-AUG-2000. WO200050633-A1. Homo sapiens (GEHO) GEN HOSPITAL CORP 99US-0121485 Location/Qualifiers 57...77 /note- "putative transmembrane domain"

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                                                                                                                      ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus crythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failuce; glomerulonephritis; vasculitis; nephriftis; end stage renal failuce; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shinsulin dependent diabetes mellitus; Crohn's disease; hypertension;
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                                                                                                                                                                                                                                                                                                                                      Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML interactor; tumour necrosis factor; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                      A human BCMA protein, a B cell protein related to TACI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY94001 standard; Protein; 184 AA.
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Pred. No. 1.3e-95;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human BCMA protein, a B cell protein crelated to transmembrane activator and CAMI-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNR) receptor. The extracellular TCC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used for inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used contained the activated or resting B lymphocytes, effector T-cells, or with activated or resting B lymphocytes, effector T-cells, or with activated or resting B lymphocytes, effector T-cells, or with activated or The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthitis. The ztnf4 activity and BR43x2. TACI or BCMA receptor-ligand engagement is associated with casthma, bronchitis, emphysema, end stage renal failure, capharans, multiple myelomas, lymphomas, light chain neuropathy, neoplasms, multiple myelomas, lymphomas, light chain neuropathy, repair capharans, multiple myelomas, lymphomas, light chain neuropathy, and light versus host disease, inflammation, insulin dependent consection, graft versus host disease, inflammation, insulin dependent consection, graft versus host disease, loint pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, tennols or entagenists or antagenists can be used to treat hypertension, renal artery consections or antagenists can be used to treat hypertension, renal artery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                 AAE09241 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stenosis,
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Pred. No. 1.3e-95;
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19-NOV-2001

(first entry)

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Matches 184
                                                                                                                                                                                                                                                                                                                                                                The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2000;
22-AUG-2000;
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TNFR;
             AAE00506 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                        BCMA protein.
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                                                                                                                                                                                                                          GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
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DB; AAD15902.
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                                                                                                                                        YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
                                                                                                                                                                             GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
                                                                                                   ISAR 184
                                                                                                                           YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
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                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                                                                                                                 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour necrosis factor; TALL-1; APRIL; TNF
BCMA; therapy; cancer; leukaemia; myeloma;
disease; rheumatoid arthritis; multiple scl
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0182938
2000US-0226986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dodge KH,
                                                                                                                                                                                                                                                                            100.0%; Score 964; DB 22; 100.0%; Pred. No. 1.3e-95; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
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                                                                                                                                                                                                                                                   APRIL-R and The present : BCM protein.
                                                                                                                                                                                                                                                                        A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as a cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus crythematosus-SLE); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, inmunosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HTV), and for treating, suppressing or altering an immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-1999;
11-FEB-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation such as cancer or carcinoma, comprises administering composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) antagonist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method of treating a mammal for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schneider P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                       Sequence
MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
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APOTECH R & D
                                                                                                                             Similarity
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                                                                                                                                                                                                       184
                                                                                                        Conservative
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2000US-0215688
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                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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                                                                                                   Score 964; DB 22;
Pred. No. 1.3e-95;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BCMA)
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RESULT 5
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ID AAB60698
XX AAB60698
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XX Huma
DT 22-N
DX Huma
KW Huma
KW B-C6
KW Immu
KW B-C6
KW Jymp
OS Homc
XX Home
XX 11-1
PN W02(
XX 11-1
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related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
                                                                                                                                                                                                                                                                                                      The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-AUG-1999;
11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension renal disorder; lmmunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; B-cell carcinoma; leukaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
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(APOT-) APOTECH R & D
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; 2000US-0181684.
; 2000US-0183536.
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RESULT 6
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                                                                                                   06-MAY-1999;
01-MAY-2000;
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                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                Human B cell maturation factor (BCMA) protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY71979 standard;
                                                                                                                                                                                                                                                                                                                                                          Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
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DB; AAD02125.
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nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.
                                                                                                                                                   Human; Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful in diagnostic assays.

The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not by brain, muscle, heart, lung, kipancreas, testis and placenta. BCMA mRNA is absent in the pro-Blymphocyte stage but its expression increases with B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocyte proliferation, used autoimmune disorders -
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Best Local
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28-JUN-2001;
29-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                          communication. The present sequence represents a protein given in the exemplification of the present invention.
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ISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated human tumor necrosis factor receptor polypeptide, 12, useful for treating autoimmune disorders, emphysema, em
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2001US-301715P.
2001US-315565P.
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Pred. No. 1.3e-95;
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AAE15484
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                                                        CC The invention relates to a method for inhibiting TACI (transmembrane CC activator and intracellular CAML interactor) and/or B cell maturation CC protein (BCMA) activity in a mammal. The method comprises administering CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF CC Edmily ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region CC of TACI or BCMA. The method is useful for inhibiting activity of TACI CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell CC lymphoproliferative disorders, one or more solid tumours such as lung, CC gastrointestinal, pencreatic or prostate tumour. APRIL, BCMA and TACI CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC dermatitis, respiratory allergic disease (astima, hypersensitivity lung Cdiseases), drug and insect sting allergy, inflammatory bowel disease (Crobn's disease, colitis), scleroderma, autoimmune disease (multiple colerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with lengocyte infiltrarion of the sign or rozane The processor sconcerns.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
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family ligand
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2001US-0214591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Cysteine-rich co
is specifically claimed
the specification"
52..72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 5..38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BCMA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
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                                                  or
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Sequence

181

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The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory

member of

Example 1; Fig

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59pp;

English

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RESULT 9
AAB60700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                   17-AUG-1999;
11-FEB-2000;
18-FEB-2000;
                                                                                Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
                                                                                                                                                                                                                                                                                                                                                immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoprolliferative disorder; hypertension, renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; archiversive plomeronephritis;
                                                                                                                         N-PSDB;
                                                                                                                                                         Thompson
                                                                                                                                                                                      (BIOJ )
                                                                                                                                                                 MacKay F,
                                                                                                                                                                                                                                                             16-AUG-2000;
                                                                                                                                                                                                                                                                                 22-FEB-2001.
                                                                                                                                                                                                                                                                                                      WO200112812-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB60700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB60700 standard;
                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                               Human BAFF-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-2001
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APOTECH R &
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                                                                     homolog
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2000US-0181684.
2000US-0183536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                 BAFF receptor; TNF family; immunoregulatory d disorder; B-cell growth inhibitor; BCMA;
                                                                                                                                                                                                                                                                                                                                            therapy; cancer; tumour;
                                                                                                                                                                                      R & D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BAFF-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                                                                                                                      SA.
                                                                                                                                                                 Ambrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence encoded by A plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 950;
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                                                                               comprising receptor or anti-BAFF-R
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                                                                                                                                                                Tschopp
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                                                                                                                                                                                                                                                                                                                                           plasmid pJST535.
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                                                                                                                                                                 Schneider
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                                                                                                                                                                ٦,
                                                                                                                                                                                                                                                                                                                                                                                              hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                            agent;
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RESULT 10
AAB08844
ID AAB088
XX AB08
XX AB08
XX D2-JA
DT 02-JA
DT 02-JA
CX BCMA;
KW BCMA;
KW anti-
KW rheum
OS Mus m
XX KW rheum
XX KW AUS MUS M
XX WO200
XX WO200
XX WO200
XX WO200
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XX WO200
XX GEHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-c cell-induced B-cell growth and maturation, and immunoglobulin production, cc cell-induced B-cell growth and maturation, and inmunoglobulin production, cc and in the treatment of autoimmune disorders. B-cell lymphoproliferative c disorders, hypertension and renal disorders. B-cell lymphoproliferative c disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV c fifther treatment of the BAFF-R c fifther treatment of the BAFF-R fifther fifther treatment of the BAFF-R fifther fifther treatment of the BAFF-R fifther fif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                         BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory resp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB08844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB08844 standard; peptide; 185
                                             24-FEB-1999;
                                                                                    24-FEB-2000; 2000WO-US04925
                                                                                                                                                                             WO200050633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of murine BCMA polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agent, and also plays a
  (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTVEECT - -
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157; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shorter than that given in AAB60698
                                                                                                                                                                                                                                                                                                                                                    death gene;
arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·CIKSKPKVDSDHCFPLP···
                                             9908-0121485
                                                                                                                                                                                                                                           Location/Qualifiers 47..72
                                                                                                                                                                                                                      /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.6%;
                                                                                                                                                                                                                                                                                                                                                    inflammatory bowel disease;
                                                                                                                                                                                                                    "putative transmembrane domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           role in the development of hypertension and
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Pred. No. 2.7
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                                                                                                                                                                                                                                                                                                                                                    septic shock
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                                                                                                                                                                                                                                                                                                                                                                           response;
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RESULT 11
AAY71980
ID AAY719
XX AAY71
XX AAY71
XX AAY71
XX AAY71
XX Wurin
DE Murin
XX Murin
KW Tumou
KW Tumou
KW Throm
K

Murine 28-MAR-2001 AAY71980

B cell maturation factor (BCMA) protein.

(first entry)

Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatorid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;

thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation post-streptococcal glomerulonephritis; polyarteritis nodosa.

proliferation;

밁 õ В

179 178 119

EKPTHTR 185

EKSISAR 184

EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM

178

AAY71980 standard; Protein;

185

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                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                            used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell degene and reporter gene, and determining alteration in reporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence
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                                                                                                                                                                                                                                                                                         Sequence
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                    120
                                                                              64 LIISLAVEVLMELLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
                                                          59
                                                                                                                                                                                                               Local Similarity 62.6 les 117; Conservative
                                                                                                                                  1 MAQQCEHSEYEDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT
                                                                                                                                                         4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILMTCLGLS
EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-558405/51.
                                                          LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          necrosis
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                                                                                                                                                                                                                                                                                              185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quence represents a BCMA (not defined) polypeptide. factor (NF)-kB activator. The method of the inventi
                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                 59.3%;
                                                                                                                                                                                                                 21;
                                                                                                                                                                                                             Score 572; DB 21;
Pred. No. 2.1e-53;
21; Mismatches 41,
                                                                                                                                                                                                                                                 Length 185;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                 8
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCMA
on is
                    177
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for

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RESULT 12
AAE15490
ID AAE15
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AC AAE15
XX
DT 12-MA
XX
DE Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC molecules, proteins (Including homologues), and their antibodies. The CC invention in particular relates to methods for regulating the CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell CC maturation factor) to regulate monocyte, macrophage and B lymphocyte CC mediated immune responses. TALL-1 protein is useful for identifying CC compounds that regulate B lymphocyte protein is useful for identifying CC crating B lymphocyte associated autoimmune disorders like rheumatoid CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, CC post-streptococcal glomerulonephritis, or polyarteritis nodosa. CC The TALL-1 protein and its corresponding nucleic acid sequence are also CC useful in diagnostic assays.
CC The TALL-1 protein sequence is a murine B cell maturation factor (BCMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
Mouse B cell maturation (BCMA) protein.
                                   12-MAR-2002
                                                                 AAE15490
                                                                                          AAE15490 standard; Protein; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to Tumour Apol-related Leucocyte expressed Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 37; Page 107-108; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders -
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01-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                     MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58
                                                                                                                                                                                                                                                                                        LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL 118
                                                                                                                                                                          EKPTHTR
                                                                                                                                                                                                    EKSISAR
                                                                                                                                                                                                                             EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM 178
                                                                                                                                                                                                                                                                                                        LIISLAVFYLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILDRGL 119
                                                                                                                                                                                                                                               EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
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                               (first entry)
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200005-0201012
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                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 572; DB
Pred. No. 2.1e
21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
.1e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      necrosis factor (TNF) and
1 (TALL-1) nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 185;
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Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
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27-JUN-2000; 2000US-214591P.
14-MAY-2001; 2001US-0214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TWF; lymphoproliferative disorder; thmour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colifis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
                                                                                                                                                                                                                                                                           family ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crohn's
                                                                                                                                                                                                                                                                                                                                    2002-066686/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       's disease; scleroderma; autoimmune disease; multiple sclerosis; immunodeficiency virus; HIV; systemic lupus erythematosus; cano
                                                                                                                                                                                                                                                                                                                                                           Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arthritis; atherosclerosis
                                                                                                                                                                                                                                                    English
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CC The invention relates to a method for inhibiting TACI (transmembrane CC activator and intracellular CAMI interactor) and/or B cell maturation CC protein (BCMA) activity in a mammal. The method comprises administering CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF CC family ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region CC of TACI or BCMA. The method is useful for inhibiting activity of TACI CI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI CC antagonists are useful for treating inflammation and immune function CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC cermatitis, respiratory allergic disease (asthma, hypersensitivity lung CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer CC is mouse BCMA protein. is mouse BCMA protein.

Sequence 185 AA;

Query Match

Local

Similarity

Length 185;

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                                                                                                      Вb
                                                                                                                                                        Matches
     119
                           120
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LIISLAVFVLMF1LRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
                                                                                                 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT
                                                                                                               MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVINSVKGTNAILWTCLGLS
                         EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI
                                               LYLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL
                                                                                                                                                       Conservative
                                                                                                                                                                  59.3%;
                                                                                                                                                      21;
                                                                                                                                                               Score 572; DB 23; Pred. No. 2.1e-53;
                                                                                                                                                      Mismatches
                                                                                                                                                    Indels
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                                                                                                                                                  Gaps
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Q

178

EKSISAR

184

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RESULT 13
AAE15501
ID
AAE15501
XX
Human
XX
Human
XX
Human
XX
Human
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Human
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AAE150
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AAE15
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                                                                                                                                                         protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (67), a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic diseases, drug and insect sting allergy, inflammation and immune function solidease, colitis), scleroderma, autolimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA cysteine-rich extracellular region.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNN; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
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27-JUN-2000; 2000US-214591P.
14-MAY-2001; 2001US-0214591.
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                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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33.5%;
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Score 323;
Pred. No.
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DB 23;
3e-27;
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RESULT 14
AAE15491

ID AAE15
XX AAE15
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                                                                                       cc activator and intracellular CAML interactor) and/or B cell maturation cc protein (BCMA) activity in a mammal. The method comprises administering ca specific binding partner for APRIL (G70, a tumour necrosis factor TNR cc family ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI cand/or BCMA in a mammal which is useful for treating B-cell or T-cell cc lymphoproliferative disorders, one or more solid tumours such as lung, cc gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI cc liseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic cd diseases, drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimune disease (miltiple cc sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, concer with leucocyte infiltration of the skin or organs. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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27-JUN-2000;
14-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for inhibiting TACI (transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 11; 94pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; atherosclerosis; mouse.
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                                                                 is human-murine B cell maturation protein (BCMA) consensus sequence.
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2000US-214591P.
2001US-0214591.
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                                                                                                                                                                                                                                                                                                                             Chimeric - Chimeric -
Treating a mammal for a condition associated
                              WPI;
                                                                                              11-FEB-2000;
30-JUN-2000;
                                                Schneider P,
                                                                                                                 06-OCT-1999;
                                                                                                                                   05-OCT-2000; 2000WO-US27579
                                                                                                                                                                                                                Doma in
                                                                                                                                                                                                                                                                                                                                                                     B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HTV; human immunodeficiency virus; TNF; murine
                                                                           (BIOJ )
                                                                                                                                                       12-APR-2001.
                                                                                                                                                                        WO200124811-A1
                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                       Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
                                                                   (APOT-)
                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                tumour necrosis factor; B cell maturation
                                                                                                                                                                                                                                                                                                                                                        immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BCMA-Immunoglobulin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE00507;
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                            2001-266242/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A----FFLLRK-----ELKDE------GSLAL------RGD---IPR-LEYTVEECTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96;
                                                                BIOGEN INC.
APOTECH R & D SA.
                    AAD03847
                                                                                                                                                                                                                                                                                                                              Mus
                                                                                             99US-0157933.
2000US-0181807.
2000US-0215688.
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                              Thompson
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                                                                                                                                                                                                                                                                                                                             sp.
                                                                                                                                                                                                            /note=
24..302
                                                                                                                                                                                                                                                                    /label= Signal_peptide
/note= "Derived from mu
23.302
                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                   /label= Mature_human_BCMA_IgG_Fc_fusion_protein
23..75
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                           /note-
                                                                                                                                                                                                     'label-
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                                                                                                                                                                                         "Derived from human BCMA"
                                                                                                                                                                                                                      "Derived from
                                                                                                                                                                                                                                        "Derived
                                                                                                                                                                                                                                                                                                                                                      Fc region.
                                                                                                                                                                                                   Cysteine_rich_domain
                                               Cachero
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fc region fusion construct.
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Pred. No. 1.3
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                                              Τ,
                                                                                                                                                                                                                     human IgG
                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                            murine Ig kappa sequence*
                                              Ambrose
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7;
                                                                                                                                                                                                                                                                                                                                                                protein;
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cell
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                                                                                                                                                                                                                                                                                                                                                                        murine;
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Query Match
Best Local S
Matches 81
                                                                                                                               prostate carcinoma, and other carcinomas whose prollieration is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-prolliferative disorders, immunosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HIV), and for treating, suppressing or altering an immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is a fusion construct containing human APRIL-R also referred as BCMA or BCM protein, Fc region of human immunoglobulin G (IGG) and a signal sequence from murine Ig kappa cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation such as cancer or carcinoma, comprises administering composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) antagonist -
                                                                                                302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85pp; English
                  29.78;
                                      DB 22;
                                         Length
                                         302;
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Ъ Ş ₽ ş Q 망 밁 Ş 114 165 121 82 19 24 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120 GKEYKCKVSNKALPA-PIEKTIS VT-YTVEECTCEDCIKSKPKVDSD------HCFPLPAMEE-----GATILVTTKTNDY-------PAPELLGGPSVFLFPPKPKDTLMISRTPE 81; Similarity 39.9 81; Conservative -CKSLPAALSATEIEKSIS -CVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 170 13; Score 286.5; DB 22 Pred. No. 2.3e-22; 3; Mismatches 54; Indels 55; Gaps 113 164

8

Search completed: November Job time: 71.2833 secs 12, 2002, 16:58:31

US-08-486-270-12
US-08-367-264-12
US-09-153-757-12
US-08-072-574-8
US-08-367-264-8
US-08-367-264-10
US-08-367-264-10
US-08-367-264-10
US-08-466-337A-18
US-08-465-887A-18
US-08-465-887A-18
US-08-188-25-891-1
US-08-332-638-42
US-08-332-638-42
US-08-332-638-42

Sequence

12, Appl 12, Appl 12, Appl 8, Appl 8, Appl 8, Appl 10, Appl 11, Appl 11, Appl 11, Appl 12, Appl 13, Appl 14, Appl 14, Appl 17, Appl 18, Appl 19, Appl

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Title:
Perfect score:
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Listing first 45 summaries
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Copyright (c) 1993 - 2002
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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  US-08-357-642A-1
US-08-416-0-656-1
US-08-810-572A-2
US-08-290-333-2
US-09-290-333-6
US-08-110-72A-6
US-09-290-333-6
US-08-660-148-5
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US-08-660-148-5
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US-08-390-411-2
US-08-39-411-2
US-08-39-411-2
US-08-39-412-2
US-08-39-4134C-2
US-08-39-400-7
US-08-39-400-7
US-08-39-400-7
US-08-353-400-36
US-08-422-542-18
US-08-765-469-18
US-08-765-469-18
US-08-72-99-11A-8
US-08-072-574-12
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e 9,
                                                      ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-357-642A-1
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US-08-357-642A-1
                                                                                                                                                           REFERENCE/DOCKET NUMBER: 32,327;
REFERENCE/DOCKET NUMBER: 209/(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08357642A Patent No. 5837524
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 31.5" DISKETTE, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,642A
FILING DATE: December 15, 1994
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: December 15, 1994
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sima Lev
APPLICANT: Joseph Schlessinger
TITLE OF INVENTION: PYK2 RELATED PRODUCTS
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                     LENGTH:
TYPE: a
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633 West Fifth Street
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Score 79.5; Pred. No. 2

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Length 1009;

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Database :

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                                                                                                                                                                                        Query Match
                                                                                                                                                           Matches
                                                                                                                                                                            Best
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                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No. 58378
                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: December 15
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: JOSEPH SCHLESSINGER TITLE OF INVENTION: PYK-2 RELATITILE OF INVENTION: METHODS
                                        306 RSIRCLPL---EEGQAVL 320
                                                                                            249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                   139 DSDHCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 955-0440
TELEX: 67-3510
RMATION ECT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/460,626 FILING DATE: June 2, 1995 CLASSIFICATION: 435
                                                                                                                                                                       Local
                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                       EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
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                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                           1009
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suite 4700
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                              489-1600
                                                                                                                                                                      8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08/357,642
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                                                                                                                                                     9;
                                                                                                                                                                    Score 79.5; DB 2; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                         211/121
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                                                                                                                                                      Pred. No. 2.5;
9; Mismatches
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                                                                                                                                                                                  Length 1009;
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                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: N
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VON Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
 210 QDH-----AMEAGSPVSTSPEPVETC
                                                             152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
                             140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                                                                                                  108 ---RTGDEIILPRG---
                                                                                                                                     93
                                                                                                                                                                       66
                                                                                                                                                                                              34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                       Local Similarity les 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 28-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                             8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
                                                                                                                                                              I-----SLAVFVLMFL------LRKISSEPLKDEFKNTGSGLLGMANIDLEKS----

    Application US/08810572A
    5969102

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                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                          N-terminal
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19.9%;
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                                                                                                                                                                                                                                                                  Score 78.5; DB
Pred. No. 0.56;
5; Mismatches
230
                                                                                                -LEYTVEECTCEDCIKSKP----KVD 139
                                                                                                                                                                                                                                                                    73;
                                                                                                                                                                                                                                                                                                  Length 293;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                                                                Gaps
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RESULT 4 US-09-290-333-2

Sequence 2, Application US/09290333 Patent No. 6316222 GENERAL INFORMATION:

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                                                                                                           RESULT 5
US-08-179-481-2
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                                                     Sequence 2, Application US/08179481 Patent No. 5624816 GENERAL INFORMATION:
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                                    APPLICANT:
                     APPLICANT:
PPLICANT:
                                                                                                                                                                                     210
                                                                                                                                                                                                                       140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                                                                                                                                                                                                                                                          152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                   93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                           34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS OF CAME, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bram, Richard J.
                                                                                                                                                                                     QDH-----AMEAGSPVSTSPEPVETC 230
                                                                                                                                                                                                                                                                                               ---RTGDEIILPRG---
                                                                                                                                                                                                                                                                                                                                                                      I-----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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CARRAWAY, KERMIT L.
CAROTHERS CARRAWAY, CORALIE A.
FREGIEN, NEVIS L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%; score 78.5; DB 4; Length 293; 19.9%; Pred. No. 0.56;
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
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RESULT 6
US-07-717-331F-2
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REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 2007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           Sequence 2, Application US/07717331F Patent No. 5484905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatability I
NUMBER OF SEQUENCES: 9
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ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 28-DEC-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                            STREET: 25 C
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                                        ZIP:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IE
                                                                                         ADDRESSEE: Yallwan - ADDRESSEE: 25 Skytop Drive
                                                                                                                                                                                                                                                                                                                                                                                                                          99 MANIDLEKSRTGDEIILPRGLEYTVEECTCEDCI 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC-----NASVTNSVKGT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                        VWNDNPE-----DDFRMPNG--STIPSNTSEETL 193
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                                                                        Connecticut
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                                                         USA
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                                                                                                                              Yahwak & Associates
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Encoded At The Self-Incompatability Locus
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COMPUTER: Macintosh OPERATING SYSTEM: M

MS-DOS

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US-09-232-160-18
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MOLECULE TYPE: peptide
US-07-717-331F-2
                                                                                                                                                                                                     APPLICANT: James Gilmore
APPLICANT: James Gilmore
APPLICANT: James Gilmore
APPLICANT: Susan G. Stuart
APPLICANT: Laura Stuve
ITILE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: PA-0003 US
CURRENT APPLICATION NUMBER: US/09/232,160
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL PROGram
SEQ ID NO 18
LENGTH: 154
                                                                                         Best
                                                                                                           Query Match
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Best Local
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                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE: -
                                                                                                                                                            OTHER INFORMATION: 1299627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 857 amino acids
TYPE: amino acid
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FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 FSSCNKL 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 NDYCKSL 168
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                               13 YFDSLLHAC-IPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCLG----LSLIIS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 CKKRCISD---CNCTAFANADIRNG--GSGCVIWTERLEDIRNYATDAIDGODLYVRLAA 434
        23
                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.8%; Score 75; DB 1; Length 857; Local Similarity 17.6%; Pred. No. 6.6; hes 33; Conservative 30; Mismatchec 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 ------CLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 CQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: George M. Yahwak
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
YADDCLAQCGKDCKSYCCDGTTPYCCSYY -- AYIGNILSGT-AIAGIVFGIVFIMGVIAG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCF----PLPAMEEGATILVTTKT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADIAKKRNASGKIISLTVGVSVLLLLIMFCL-----WKRKQKRAKASAISIANTQRNQ 487
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5. 6368794
                                                                                      Similarity
                                                                        Conservative
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                                                                                    7.3%;
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                                                                                  Score 70.5;
Pred. No. 1
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                                                                    Mismatches
                                                                                      .9;
                                                                                                    DB 4;
                                                                    52;
                                                                                                    Length 154;
                                                                  Indels
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                                                               Gaps
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HYPOTHETICAL: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE:
ORGANISM: Homo
US-08-810-572A-6
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Best Local Similarity
Matches 15; Conserve
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US-08-810-572A-6
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                                                                                Sequence 6, Application Patent No. 6316222 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/810, FILING DATE: 28-FEB-1997 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., David A. REGISTRATION UMBER: 26,742 REFERENCE/DOCKET NUMBER: 1340-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND
NUMBER OF SEQUENCES: 11
CORRESPONDENCE: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                               34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                           8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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VON BULOW, GOTZ
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AN
                                                                 APPLICANT: Bram,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hackensack
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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11 Hackensack Ave, Continental Plaza, 4th
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                                                                 Richard J.
                                                                                                                  US/09290333
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                                                                                                                                                                                                                                                             Score 69.5; DB Pred. No. 2.8; 14; Mismatches
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                                                                                                                                                                                                                                                                                             DB 2;
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             AND METHODS OF
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                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                       APPLICANT: Sharp, Re APPLICANT: Snyder, Y TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                       CUNTRY: United States of America ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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HYPOTHETICAL: NO
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                                                                                                                           Indianapolis
Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 166 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: David A.
                                                                                                                                                                                                                                   Snyder, Yvonne M.
VENTION: EXCITATORY AMINO RECEPTOR PROTEIN
                                                                                                                                                                                                                                                                                      Burnett, J. P.
Mayne, Nancy G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                         RELATED NUCLEIC
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25.0%; Pred. No. 2.
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             Version
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US-08-660-148-5
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           PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                           APPLICATION NUMBER: FILING DATE:
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                                             CLASSIFICATION:
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; MOLECULE TYPE: protein US-08-660-148-2
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Best Local Similarity 24...
49; Conservative
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APPLICANT: Burnett
APPLICANT: Mayne,
APPLICANT: Sharp,
APPLICANT: Snyder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (317) 276-38 INFORMATION FOR SEQ ID NO:
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NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1180 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (317) 276-0756
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APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                       APPLICANT: SNYGER, YOONNE M.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 -- LLATLFVTVVFIIYRDTPVVKSSSRELC-----
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                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSLIISLAVFVLMFLLR-----KISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILP 116
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                                                                                                                     46285
                                                                                                                                                                         Indianapolis
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                                                                                                                                                         Indiana
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Lilly Corporate Center
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                                                                                                                                   United States of America
                                                                                                                                                                                                                                                                                                                             Burnett, J. P. Mayne, Nancy G. Sharp, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Pred. No. 4
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14;

US/08/282,853

US/08/660,148

Version

#1.25

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHARACTERISTICS:
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US-08-459-568-2
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NAME: Gaylo, Paul J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-9419

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 276-3861

TELEFAX: (317) 276-3861

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

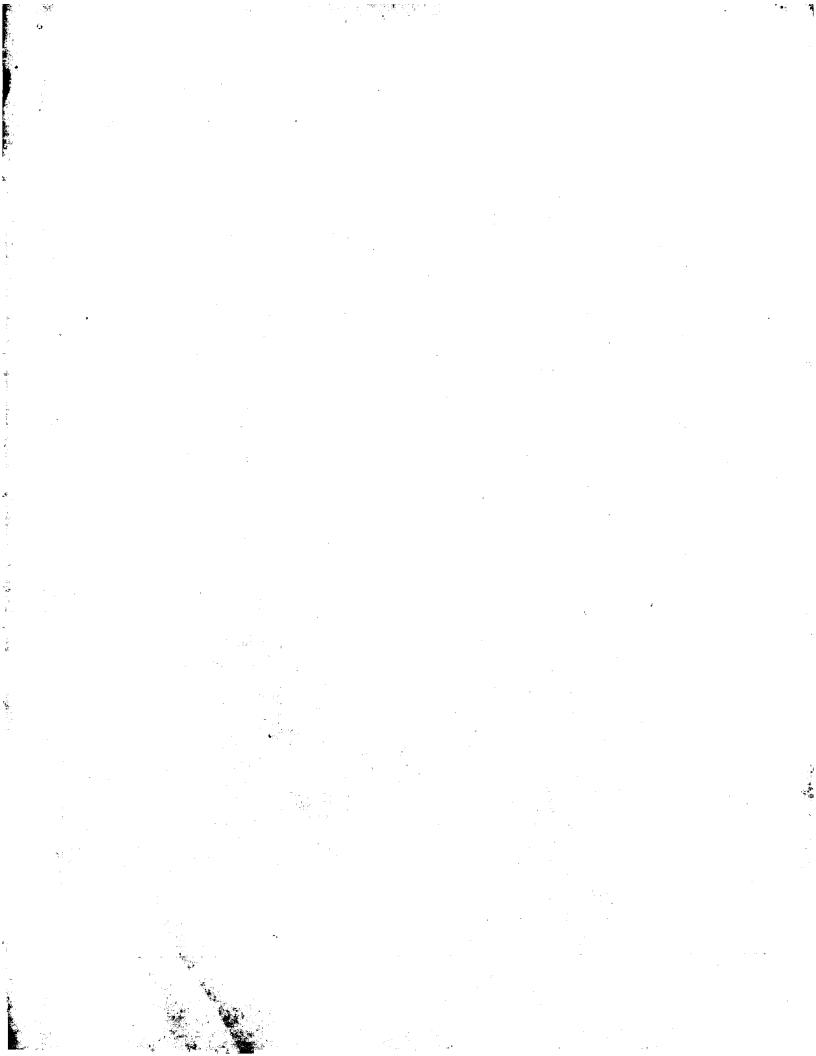
LENGTH: 1212 amino acids
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Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: Huang, Shi
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Best Local Similarity 24.6%;
Matches 49; Conservative 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Retinoblastoma Protein - Interacting
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CITY: San Diego
STATE: California
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TOPOLOGY: linear
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; Pred. No. 47;
21; Mismatches 52; Indels 77
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Qy 34 PLTCQRYCNASYTNSVKGTNAI : : : : Db 598 PYTVEITQNIKSTQV- QY 94 SGLLGMANIDLEKSRTGDEIIL ::	Query Match 7.2%; Best Local Similarity 21.7%; Matches 34; Conservative	TELEPHONE: (619) 535-9901 TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1706 amino acids TYPE: amino acid TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-399-411-2	APPLICATION NUMBER: US/08/3 FILING DATE: 06-MAR-1995 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: DELECOMMUNICATION INFORMATION:		RESULT 13 US-08-399-411-2 Sequence 2, Application US/08399411 Patent No. 5831008 GENERAL INFORMATION: APPLICANT: Huang, Shi TITLE OF INVENTION: Retinoblastoma Protein - TITLE OF INVENTION: Zinc Finger Proteins NUMBER OF SEQUENCES: 93 CORRESPONDENCE ADDRESS: ADDRESSEE: Campbell and Flores STREET: 4370 La Jolla Village Drive, Suite	627 148 675	atches 34 598	WOLECULE TYPE: protein US-08-459-568-2 Query Match Best Local Similarity 21 7%:
PUTCORYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG : :: :: :: :: :: :: : :	Score 69.5; DB 2; Length 1706; Pred. No. 77; 22; Mismatches 44; Indels 57;	9001 49 2: 1ds	UMBER: US/08/399,411 06-MAR-1995 08: 530 N: 530 INFORMATION: 11, Cathryn A. 11, Cathryn A. 11, Cathryn A. 12, Cathryn A. 13,815 VUMBER: 91,815 VUMBER: 91,815 NINFORMATION:	isk attble DOS/MS-DOS lease #1.0, Version #1.25	08399411 inoblastoma Protein - Interacting c Finger Proteins nd Flores Village Drive, Suite 700		LWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNT LWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNT :::: ::	SC
93 626 147	Gaps 7;					147 674		

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RESULT 15
US-09-586-472-2
; Sequence 2, Application US/09586472
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Patent No. 606923
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                          148 AMEEGATILVTTKTNDYCK----SLPAALSATEIEK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Diego
STATE: California
                                                                                                                                                                                             94 SGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP------KVDSDHCFPLP 147
                                                                                                                                                                                                                                                             34 PLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0: FILING DATE: 06-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P-LJ 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMEEGATILVTTKTNDYCK-----SLPAALSATEIEK 179
                                                                                                                                                           ----NCESKKRRTASPPVLPKIKTETESDSTAPSCSLSLPLSISTAEVVSFH-----
                                                                                          -KEKG--VYLSSKLKQLLQTQDKLTLPAGFSAAEIPK 708
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                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                              7.2%;
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Zinc Finger Proteins
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Village Drive,
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Pred. No. 77;
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Search completed: November 12, Job time: 28.2704 secs
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GENERAL INFORMATION:
APPLICANT: Huang, Shi
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                       Best
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                                                                                                         148 AMEEGATILVTTKTNDYCK----SLPAALSATEIEK 179
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                                                                                                                                                                                                                                                            34 PLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/292,683 FILING DATE: 18-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Retinoblastoma Protein - Interacting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                         -KEKG--VYLSSKLKQLLQTQDKLTLPAGFSAAEIPK
                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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4370 La Jolla Village Drive,
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Pred. No. 77;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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964
  92612 segs, 14418503 residues
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            /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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3: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	μ	12	11	10	9	80	7	6	U	4	Ĺ	N	1	No.	Result
70	70.5	70.5	78	78.5	78.5	78.5	79.5	79.5	104	187	201	201	284	286	311.5	323	572	950	Score	
7.3	7.3	7.3	8.1	8.1	8.1	8.1	8.2	8.2		19.4					32.3	33.5	59.3	98.5	Match Length	Query
180	1203	397	291	293	293	293	1009	293	21	281	81	34	51	283	117	58	185	181	Length	
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US-09-780-717-11	US-10-027-923-5	US-09-854-864-18	US-09-779-050A-43	US-09-961-376-2	US-09-854-864-14	US-09-879-919-22	US-08-987-689A-2	US-09-779-050A-42	US-09-854-864-8	US-09-854-864-10	US-09-854-864-13	US-09-854-864-7	US-09-854-864-6	US-09-854-864-9	US-09-854-864-12	US-09-854-864-21	US-09-854-864-11	US-09-B54-864-5	ID	
_	Sequence 5, Appli	Sequence 18, Appl		Sequence 2, Appli	Sequence 14, Appl	Sequence 22, Appl	Sequence 2, Appli	Sequence 42, Appl	Sequence 8, Appli	Sequence 10, Appl	Sequence 13, Appl	Sequence 7, Appli	Sequence 6, Appli	9	Sequence 12, Appl	Sequence 21, Appl	Sequence 11, Appl	Sequence 5, Appli	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
64.5	64.5	64.5	65	65	65.5	65.5	65.5	65.5	66	6 6	66	66.5	67	67	67.5	67.5	68.5	69	69	69	69.5	69.5	69.5	70	2
6.7	6.7	6.7	6.7	6.7	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.9	7.0	7.0	7.0	7.0	7.1	7.2	7.2	7.2	7.2	7.2	7.2	7.3	1.3
418	195	195	386	386	3034	3034	798	728	376	317	317	67	1113	320	664	37	305	774	772	324	1212	166	59	836	ZRI
9	10	10	12	12	10	10	12	10	10	10	9	10	10	10	10	9	10	10	10	10	12	10	10	10	T
US-09-886-429-2	US-09-224-683-44	US-09-005-243-44	US-10-105-929-6	US-10-039-785-4	US-09-737-149-30	US-09-737-149-25	US-10-078-929-192	US-09-908-322-2	US-09-735-787-4	US-09-844-908-1	US-09-844-988-1	US-09-854-864-16	US-09-836-470B-3	US-09-797-481-8	US-09-780-525-2	US-09-779-050A-45	US-09-771-730-119	US-09-815-837-72	US-09-815-837-74	US-09-797-481-7	US-10-027-923-4	US-09-854-864-15	US-09-854-864-20	US-09-925-301-1088	US-09-780-717-44
Sequence 2, Appli	Sequence 44, Appl	Sequence 44, Appl	Sequence 6, Appli	Sequence 4, Appli	Sequence 30, Appl	Sequence 25, Appl	Sequence 192, App	Sequence 2, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 16, Appl	Sequence 3, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 45, Appl	Sequence 119, App	Sequence 72, Appl	Sequence 74, Appl	Sequence 7, Appli	Sequence 4, Appli	Sequence 15, Appl	Sequence 20, Appl	Sequence 1088, Ap	Sequence 44, Appl

ALIGNMENTS

US-09-854-864-5

Sequence 5, Application US/09854864 Patent No. US20020081296A1

GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                            EILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 5
LENGTH; 181
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                     Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: THEILL, LA APPLICANT: YU, GANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI
184 R 184
                                     121
                                                                                                            61
                                                                                                                         64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
                                                                                                                                                                                                                                                Match 98.5%; Score 950; DB 10; Local Similarity 100.0%; Pred. No. 2e-89; les 181; Conservative 0; Mismatches 0;
                                                                                                                                                                           EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
                                                                                                        LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV
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US-09-854-864-11
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                                                                                         SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 58
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
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Best Local Similarity
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GENERAL INFORMATION:
  Query Match
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                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI FILE REFERENCE: A-686B
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
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FILE REFERENCE: A-686B
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                                                                               TYPE: PRT
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Pred. No. 4.8e-51;
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  323;
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; PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
: PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 9
: LENGTH: 283
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-854-864-9
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
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Best Local Similarity
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
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FILE REFERENCE: A-686B
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
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TYPE: PRT
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pred. No. 7.5e-25;
4; Mismatches 7;
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US-09-854-864-6
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
FILE REFERENCE: A-686B
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SEQ ID NO 6
LENGTH: 51
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CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
                                                     CURRENT APPLICATION NUMBER: US/09/854,864 CURRENT FILING DATE: 2001-09-11 PRIOR APPLICATION NUMBER: US 60/204,039 PRIOR FILING DATE: 2000-05-12 PRIOR APPLICATION NUMBER: US 60/214,591 PRIOR APPLICATION NUMBER: US 60/214,591 PRIOR FILING DATE: 2000-06-27
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                                      NUMBER OF SEQ ID NOS: 31
                    SOFTWARE: PatentIn version 3.1
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les 51; Conservative
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Pred. No. 8.8e-22;
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US-09-854-864-7
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US-09-854-864-13
                                                         ; ORGANISM: Mus
US-09-854-864-10
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US-09-854-864-13
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Matches
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LENGTH: 81
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/854,864 CURRENT FILING DATE: 2001-09-11 PRIOR APPLICATION NUMBER: US 60/204,039 PRIOR FILING DATE: 2000-05-12 PRIOR APPLICATION NUMBER: US 60/214,591 PRIOR FILING DATE: 2000-06-27
                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
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                                                                                               LENGTH: 28
TYPE: PRT
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100.0%; Pred. No.
live 0; Mismatch
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Pred. No.
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187; DB 10;
No. 9.8e-12;
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7.8e-14;
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                Length 281;
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US-09-779-050A-42
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US-09-854-864-8
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US-09-854-864-8
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US-09-779-050A-42
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Best Local
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                                                                SEQ ID NO 42
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PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
                                                                                                            CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
                                                                                NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
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             ORGANISM: Homo sapiens
                                 TYPE: PRT
                                               CENGTH:
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les 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVLTVLHQDWLNGKEYKCKVSNKALPA-PIEKTIS 171
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100.0%; Pred. No.
Live 0; Mismatch
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US-08-987-689A-2
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                Query Match
Best Local
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                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                            FILING DATE: June 2, 1995
APPLICATION NUMBER: 08/357,642
FILING DATE: December 15, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                    TOPOLOGY: 11
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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CITY: Los Angeles
CTATE: California
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ADDRESSEE: Lyon & Lyon
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TITLE OF INVENTION: PYK2 RELATED PRODUCTS AND METHODS
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                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                            TELEFAX: (213) 955-0440 TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
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                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: December 11, 1996
APPLICATION NUMBER: 08/460,626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                        linear
                                                                                                                                                                                                                                              (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER: US/08/987,689A
December 9, 1997
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Pred. No. 4;
9; Mismatches
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PRIOR APPLICATION NUMBER: 08/215,783
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-03-14
PRIOR FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 293
RESULT 14
US-09-814-864-14
; Sequence 14, Application US/09854864
; Patent NO. US20020081296A1
; Patent NO. US20020081296A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: TU, GANG
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22
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PRIOR FILLING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR FILLING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILLING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/254,875
PRIOR FILLING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/241,952
PRIOR APPLICATION NUMBER: 60/241,952
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-10-23
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TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/879,919
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/211,537 PRIOR FILING DATE: 2000-06-15
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19.9%; Pred. No. 1.1;
tive 35; Mismatches 73;
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Job time : 15.2146 secs	Search completed: November 12, 2002, 17:09:11	QDHAMEAGSPVSTSPEPVETC 230	SDHCEPLPAMEEGATILVTTKTNDYC 165	152 GLKLSADOVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSRPRQSPAKSS 209	PRG	93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
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Maximum Match 100%
Listing first 45 summaries
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S-locus-specific	T14525	N	424	7.3	70.5	45	
hypothetical	T24023	N	412	7.3	70.5	44	
hypothetical	н82933	N	188	7.3	70.5	43	
spike glycoprotei	T02768	N	660	7.4	71	42	
hypothetical prote	T10543	N	500	7.4	71	41	
protein F41H10.1	G88690	N	480	7.4	71	40	
ABC transporters	AF1207	N	473	7.4	71	39	
probable cell divi	G71331	N	414	7.4	71	38	
conse	F72334	N	227	7.4	71	37	
hypot	B71709	2	627	7.4	71.5	36	
hypot	T10350	N	105	7.4	71.5	35	
hypothetica	T10665	N	855	7.5	72	34	
hypothetical	S75097	N	416	7.5	72	33	
hypothetical	B84518	N	408	7.5	72.5	32	
hypothetical	T31144	N	243	7.5	72.5	31	
probable serine/t	A403/3	-	/33	0	/ 4	C	

ALIGNMENTS

Rilabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A. Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, A;Reference number: 843486; MUID:94218235; PMID:8165126
A;Accession: \$43486
A;Status: preliminary

is ğ

A; Molecule type: DNA A; Residues: 1-184 < LAA>

B-cell maturation factor - human R/Alternate names: BCM protein; BCMA protein; BEL protein C;Species: Homo sapiens (man) C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_C;Accession: S43486; S31208; S36661

27-Jan-1995 #text_change 21-Jul-2000

RESULT 1 S43486

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A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245 R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsap EMBO J. 11, 3897-3904, 1992 A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t A;Reference number: S31208; MUID:93010984; PMID:1396583
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A; Residues: 4-184 <LA3>
A; Cross-references: EMBL:Z14955
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A;Accession: S36661
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                                                                                     GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
                                                                                                                                                                              MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                   Score 964; DB 2;
Pred. No. 5.6e-81;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                              Length 184;
                                                                                                                                                                                                                                                                        Indels
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amino acid ABC transporter, permease component CAC3619 [imported] - Clostridium C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Caccession: C97344 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacte A;Reference number: A96900; MUID:21359325; PMID:21359325
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                                                                                                                                                                                                                                      R; Weigmann, A.; Corbeil, D.; Hellwig, A.; Huttner, W.B. Proc. Natl. Acad. Sci. U.S.A. 94, 12425-1230, 1997 A; Title: Prominin, a novel microvilli-specific polytopic A; Reference number: Z16512; MUID:98024147; PMID:9356465 A; Accession: T08881
                                                                                                                                                                                                                                                                                                                         prominin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
C;Accession: T08881
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C;Superfamily: histidine permease protein M
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                                                                                                                                   A; Experimental source: kidney C; Keywords: glycoprotein; mem
                                                                                                                                                                                      A; Residues: 1-858 <WE
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A; Residues: 1-217 < KUR>
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                                                                                                                                                                                                                      A; Status: preliminary; translated
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Best Local S
Matches 55
                                                                   Matches
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 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 DAVTPYLFAGIFYLILTTIFTGIFSK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 ALGLTYGQTMKRIILPQAIRVVIPPCGNEFIAMIKDTSLVSVITMEELLRKAQLLVSSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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                               18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 SLLHACIPCQLRCSSNTPPLTCQRYCNASV-----TNSVKGTNAI----LWTCLGL 62
                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TGDEIILPRGLEYTVEEC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLLLQLYVYYYGLPFLSDKLTMTPMKAAILGLSLNSGAYIAEIIRGGILAIDNGQFEASK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLIISLAVEV--LMFLLRKISSEPLKDEF----KNTGS-----GLLGMANIDLEKSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSLNKVIPVLLDGTRITLLLTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT
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                                                                   44;
                                                                                                                                                                                    1-858 <WEI>
                                                                 Similarity 22.7
44; Conservative
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                                                                               9.0%;
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                                                                                                                                   membrane protein
---CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
                                                                 30;
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                                                               Score 86.5; Depred. No. 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 88.5; D
Pred. No. 0.98
25; Mismatches
                                                                                                                                                                                                                        from
                                                                                                                                                                    NID:g2559003;
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                                                                                                 DB 2;
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                                                                                                                                                                    PIDN:AAB86715.1; PID:g2559004
                                                                   67;
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ATCC824
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                                                                                              Length 858;
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R;Sasaki, H.; Nagura, K.; Ishino, M.; Tobioka, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A;Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-t A;Reference number: A57434; MUID:95403356; PMID:7673154
A;Accession: A57434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Map position: 3
A:Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; C:Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1998 <CHO>
A; Cross-references: EMBL.AL096856; GSPDB:GN00061; ATSP:T24C20.
A; Cross-references: cultivar Columbia; BAC clone T24C20
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T13009
                                                                                                                                                                                                                                                                                                                                                                       protein-tyrosine kinase (EC 2.7.1.112) CAK-beta
N;Alternate names: cell adhesion kinase-beta
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T24C20.80 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Nov-1999 C;Accession: T13009
                                                                                                                                                                                                                    A; Status: preliminary
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A; Accession: T13009
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Best Local S
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nes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 QRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLVKLSSLDM--SRLGD-----RGIHFFDEGGSCNGRSSSAPGLNTGNVNIDMCGDL--M 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLPAM 149
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  8.5%;
26.9%;
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  Score
Pred.
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Pred. No. 27;
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    В2;
No.
DB
18;
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                                                                                                                                   kinase hom
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Local Similarity

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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el.
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Nielsen, E.; You, Y.; Forney, J.
J. Mol. Biol. 222, 835-841, 1991
A;Title: (Cysteine residue periodicity is a conserved A; Reference number: 20504; MUID:92106337; PMID:1766
A; Recession: T28669
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Paramecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T28669
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                                                                                                                                     A;Cross-references: GB:chr_V; PIDN:AAB54249.1; PID:g2088832; GSPDB:GN00023; CESP:R08F11 A;Note: Similar to peroxidase C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                       protein R08F11.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
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                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-773 <STO>
                                                                                                                                                                                                                                                      A; Accession: D89010
                                                                                                                                                                                                                                                                                                                                                 Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                       R; anonymous,
                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
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A; Residues: 1-2233 <NIE>
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                                                                                                                 A; Gene: R08F11.7
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                                                                          myeloperoxidase; myeloperoxidase
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Conservative
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25,1%;
                  8.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g159974; PID:g159975;
                  Score 81;
Pred. No.
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Pred. No. 45;
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91;
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Indels
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C;Keywords: ATP; phosphottansferase; tyrosine-specific protein kinase
F;423-686/Domain: protein kinase homology <KIN>
F;431-439/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-22,'G',24-150 <SA2>
A;Cross-references: GB:D45853; NID:g1000676; PIDN:BAA08289.1; PID:d1008884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 270, 21205-21217, 1222
A;Title: Cloning and characterization of cell adhesion kinase
A:Reference number: A57434; MUID:95403356; PMID:7673154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: H01067
A; Accession: G02330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 10-Apr-1996 #sequence_revision 27-Feb-1997 #text_change 17-Nov-2000
C;Accession: S60248; G02330; B57434
R;Lev, S.; Moreno, H.; Martinez, R.; Canoll, P.; Peles, E.; Musacchio, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - N; Alternate names: cell adhesion kinase-beta
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Nature 376, 737-745, 1995
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Best Local
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RESULT 9 T43251 furin (EC

3.4.21.75) -

fall armyworm

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R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak, Relch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Function: csponsi
A;Description: responsi
C;Reywords: hydrolase;
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R;Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
submitted to the EMBL Data Library, January 1996
submitted to the EMBL Data Library, January 1996
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C; Superfamily: conserved hypotheti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A64300; A; Accession: D64469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             potassium channel homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: D64469
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A:Residues: 1-1299 <CIE>
A:Cross-references: EMBL:Z68888; NID:g1167859;
A:Experimental source: clone Sfurin 6; ovary
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T43251
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U67575; GB:L77117; NID:g1591992;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-343 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation
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Best Local
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    141
                                              112 EII------DRGLEYTVEECTCEDCIKSKPKV------DSDHCF-PLPAMEEG 152
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                                                                                                                                       72 VLMFL------LRKISS--EPLKDEFKNTGSGLLGMA-----NIDLEKSRTGD 111
                                                                                                                                                                                                                                    12 EYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVF 71
                                                                                                                                                                                                                                                                                                            Local
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DVLKEEYEKYPDKFLYIVGDAKKEEVLK-KAKIDKAKGLIATLPSDADNVFLTLTARELN 199
                                                                                                                                                                                     DYFTALYFSVI-----TITTTGYGDFTPKTFLGRTLTVVYLCVGVGIVMYLFSL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALHTAPSADAAPSVAVVTIAVCAAAVGLFITVLVVLQAHSPREKKTRKTSVRG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDLEKSRTGDEIILPR-GLEYTVEECTCEDCIKSKPKVDSDH 142
                                                                                            IAEFIVEGKFEEFVRLKKMKNKIKTLKDHYIICGYGRLGKVVGEKFIEENIPFIAIDINE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --VEYSR-----LPRTDVDFTV----LTSCTDQEGPVEYEH 1289
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39; Conserv
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Pred. No. 40
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Pred. No. 1
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dek, A.
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GCS894 precursor - mouse Killer cell inhibitory receptor p91A precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #tel
                                                                                                                                                                                                                                                                                                                                                                                                                     F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-641/Product: killer cell inhibitory receptor p91A *status predicted <MAT>
F:24-18,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like
F:636-674/Domain: transmembrane *status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: JC5894
R;Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.;
J. Biochem. 123, 358-368, 1998
A;Title: Genomic structures and chromosomal location of
A;Reference number: JC5894; MUID:98218758; PMID:9538215
A;Accession: JC5894
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C;Comment: This protein function
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A; Residues: 1-841 < YAM>
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Best Local S
Matches 46
742
                                                                                                                    119
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                                    163 DYCKSLPAAL-SATEIEKSISAR 184
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                                                                            RPNPAAATQEESLYASVEDMQTEDGVELNSWTPPEED-----
                                                                                                                  -----LEYTVEECTCEDCIK----SKPKVDSDHCFPLPAMEEGATILVTTKTN 162
                                                                                                                                                                                                                                                                               SQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSL 64
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46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein function
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                                                                                                                                                                                                                                                                                                                   8.1%; Score 78; DB 22.7%; Pred. No. 35; tive 32; Mismatches
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                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                          -DLQLSSGAEEPITRKGELQK 699
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R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712 hypothetical protein F16F4.10 [Imported] - Arabidopsis thallana C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002 C;Accession: D86345 A; Molecule type: DNA A; Residues: 1-738 <S A; Status: preliminary A; Reference number: A; Accession: D86345

A;Cross-references: GB:AE005172; NID:g8920639;

PIDN: AAF81361.1;

GSPDB:GN00141

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A:Cross-references: EMBL:AL132956
A:Experimental source: cultivar Columbia;
C:Genetics:
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A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                            hypothetical protein F2K15.50 - Arabidopsis thaliana c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000 C;Accession: T45824
A; Map position: 3
A; Introns: 69/3; 271/3;
A; Note: F2K15.50
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A;Reference number: Z14407
A;Accession: T01733
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C; Accession: T01733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein A_IG002N01.31 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1
C; Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25;
                                                                                                            A; Molecule type: DNA
A; Residues: 1-522 <RIE>
                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                   A; Reference number: Z23015
A; Accession: T45824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 4
A; Introns: 112/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-968 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Scheet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_IG002N01.31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.; Maggi, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DELKEIGKAL-----LPQSTSNKALPAPATVTAEAESATATTTTVDKP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSGDSTCENKLGHFRCNCRSRYELNTTTNTCKPKGNPEY---VEWTTIVLGTTIGF-LVI 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSQNEYFDSLL-HACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLII 66
                                                                                                                                                                                                                                                                                                                                                                                                                        SSLTDSISGVFGESSDGVSVALGVAAAAGLSVFAFTEDRKQTLKQVDEFLNTKVAPKELV
                                                                                                                                                                                                                                                                                                                                                                                                --VPEPETVAATTTTVDKPVPEPEPVPEPVPVPAIEAAVAAQ 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASVTNSVKG----TNAILWTCLGLSLIISLAVFVLM------FLLRKISSEPLK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136/2; 164/3; 237/3; 356/1; 430/1; 460/2; 718/2; 752/3; 781/3; 806/3;
                 294/1; 327/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 77.5; D; Pred. No. 34; 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 77.5;
Pred. No. 45
                                                                                                                                                                                                         Database,
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                 397/3; 443/3
                                                                                                                                                                                                                          S . ;
                                                                        BAC clone F2K15
                                                                                                                                                                                                       Schaefer, M.;
, January 2000
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Search completed: November 12, Job time : 31.4292 secs

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R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, M.S.; Phillips, Phillips, C.A.; Phillips, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methyl-accepting chemotaxis protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: F72288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
F72288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: C; Genetics:
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A; Residues: 1-539 < ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A72200; A; Accession: F72288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: Arabidopsis thaliana hypothetical protein F2K15.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE001772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 SLVLACMRKTSNPDELPSLPYQYRSSSRSSLLTTGSRSDSRLLWLVK----VIWTAVILG 214
203 --NVEIEKIRSKDEI
                                                                                                                                                               150
                                              99 MANIDLEKSRTGDEI 113
                                                                                                                                                                                                                                      42 NASYTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD---EFKNTGSGLLG 98
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                               NVSMTKNIK-RNIIFF----LVVVCAAAMFIAIFTTRNLTT-PLKKLAVLVENLSHGVL- 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :AE001772; GB:AE000512; NID:g4981693; PIDN:AAD36222.1; PID:g498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lateral gene transfer between Archaea 2200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                           8.0%;
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27.0%; Pred. No. 27;
tive 18; Mismatches
215
                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                     Pred. No. 28;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Score 77;
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27;
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 539
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Maximum DB seq length: 2000000000
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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FAK2 HUMAN
T13X HUMAN
T101 FREMA
T107 RACSU
MGR5 RAT
PCK5 MOUSE
G156 PARPR
HS70 TR1RU
TLPC BACSU
MGR5 HUMAN
TAN MOUSE
G5AR RAT
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O96rj3 homo sapien
O5490 mus musculu
O94yp9 m protein t
P70600 rattus norv
Q14289 h protein t
O14836 homo sapien
O58752 methanococc
Q9et35 mus musculu
O74910 schizosacch
O10902 brassica ol
P41771 kluyveromyc
P82295 drosophila
O10331 orgyia pseu
O9zec6 rickettsia
O9wzq4 thermotoga
O9pr43 ureaplasma
P31424 rattus norv
O14592 mus musculu
P13837 paramecium
O93866 trichophyto
P39209 bacillus su
P41594 homo sapien
O88799 mus musculu
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ALIGNMENTS

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FUNCTION. FUNCTION. FUNCTION: MEDLINE=20363816; PubMed=10903733; Hatzoglou A., Roussel J., Bourgeade MF., Rogier E., Inoue J., Devergne O., Tsapis A.; "TNF receptor family member BCMA (B cell maturation) "TNF receptor-associated factor (TRAF) 1, TRAF2, and T TNF receptor-associated factor (TRAF) 1, TRAF2, and T	Kim UJ., Sneddon V.P. Mason T., Crosby M.L., ys A., Cao Y., Xu R.X., ys A., Cao Y., Xu R.X., harris P.C., Venter J. ications and other featu some 16p and 16q.", 295-308(1999). M. N. A., AND VARIANT THR- 9161: PubMed-11528522; Tsuchiya N., Fukazawa four major haplotypes a four major haplotypes ryth with systemic lupus eryt	., AND CHROMOSOMAL TRAN. blood leukocytes, and pubMed=1395583; P., Carbonnel F., Broue is A.; on chromosome 16 is fup13) translocation in a 904(1992). PubMed=8165126; PubMed=8165126; PubMed=105126; Pu	TRI7_HUMAN STANDARD; PRT; 184 AA. Q02223; Q1-JUL-1993 (Rel. 26, Created) O1-JUL-1993 (Rel. 26, Last sequence update) O1-JUL-1993 (Rel. 41, Last sequence update) TUN-2002 (Rel. 41, Last annotation update) Tumor necrosis factor receptor superfamily member 17 maturation procein). TNERSFI7 OR BCMA OR BCM. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID-9606;
., Rogier E., Madry C., maturation) associates with TRAF2, and TRAF3 and minal kinase, and p38	, Kalush F., Brandon R., Barnstead M., Cronin L., Kang HL., Mitchell S., C., Adams M.D.; c., Adams M.D.; res in 12 Mb of DNA sequence from 153. 153. 153. 153. 164. 170. 185. 186. 186. 187. 188. 188. 188. 188. 188. 188. 188	TRANSLOCATION. and Lymph node; rouet J.C., Berger R., s fused to the interleukin 2 gene in a malignant T cell lymphoma."; in a malignant T cell lymphoma."; reger R., Larsen C.J., Tsapis A.; ssed during B lymphoid cribed.";).	.e) member 17 (B-cell tebrata; Euteleostomi;

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Gross J.A., Johnston J., Mudri S., Enselman R., Dillc Madden K., Xu W., Parrish-Novak J., Foster D., Lofton A Moore M., Littau A., Grossman A., Haugen H., Foley K., Harrison K., Kindsvogel W., Clegg C.H.;
"TACI and BCMA are receptors for a TNF home"
autoimmune disease.";
Nature 404:994.000
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"APRIL and TALL-I and receptors humoral immunity.";
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REPEAT
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                                                                                                                                                                                                                                                                                            EMBL;
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SEQUENCE
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                                                                                                                                               TRANSMEM
                                                                                                                                                                                      Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell maturation protein is a receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           illy member TALL-1.";

c. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).

c. NCCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.

Promotes B-cell survival and plays a role in the regulation

humoral immunity. Activates NF-kappa-B and JNK.

SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZED BY A CHROMOSOMAL TRANSLOC WHICH INVOLVES BCMA AND IL2.
SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
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DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type III membrane protein and perinuclear Golgi-like structures.
TISSUE SPECIFICITY: Expressed in mature B-cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H.-B., Johnson H.;
                                                                                                                                                                                                                                                   1: Z14954; CAA78679.1; -...; Z29575; CAA82691.1; -...; Z29574; CAA82690.1; -...; Z29574; AB67251.1; -...; AB652772; BAB60895.1; -...
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$31209; $31209.
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                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
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translocation; Polymorphism.
EXTRACELULLAR (POTENTIAL).
SIGNAL-ANCHOR (TYPE III MEMB
                       BREAKPOINT FOR TRANSLOCATION TO INTERLEUKIN 2/BCM ONCOGENE.
BY SIMILARITY.
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CYTOPLASMIC (
TNFR-CYS.
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277AF11E2767D932
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                                                                                                                                                                                                                                                                                                                                              noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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 Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aa Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aa Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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Aa Schriml L., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Aa Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Aa Blake J., Boffelli D., Bojunga N., Carninol P., de Bonaldo M.F.,
Aa Blake J., Boffelli D., Bojunga N., Carninol P., de Bonaldo M.F.,
Aa Brownstein M.J., Bult C., Fletcher C., Frjita M., Gariboldi M.,
Aa Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Aa Lyons P., Marchboni L., Mashima J., Mazzarelli J., Mombaerts P.,
Aa Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Assaaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Aa Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
An Marchall R., Washida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
An Marchall R., Washida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 184
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088472;
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-C57BL/6J; TISSUE-Colon;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maturation protein).
TNFRSF17 OR BCMA OR
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Hayashizaki Y.;
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Mammalia; Eutheria;
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                                                                    Nature 409:685-690(2001)
                                                                                    "Functional annotation
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15-JUN-2002 (Rel. 41, Last annotation update)
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FUNCTION: Receptor for INFSF13B/BLYS/BAFF and INFSF13/APRIL. Promotes B-cell survival and plays a role in the regulation humoral immunity. Activates NF-kappa-B and JNK (By similarit SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laabi Y., Callebaut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10:1693-1702(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Spleen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
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                                                                                    full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 964; DB 1;
Pred. No. 1.3e-83;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                      mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                    collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murinae;
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                   similarity)
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>:</del> :
                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor) (B-cell maturation defect)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). STRAIN-BALB/c; TISSUE-B-cell lymphoma; MEDLINE-21442025; PubMed-11509692;
                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                       Q9D8D0;
                                                                                                                                                                                                                                                                                                                                                                           T13C_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
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                                                                                                                                                                                                 TNFRSF13C OR BAFFR OR BCMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
SUBCELLULAR
ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type III membrane protein a ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) produced by alternative splicing.
TISSUE SPECIFICITY: Detected in spleen, thymus, heart, and at lower levels in kidney and lung. SIMILARITY: CONTAINS 1 THER-CYS REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:1343050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKSISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKPTHTR
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117; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  requires a license agreement (So
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immune response;
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CYTOPLASMIC (POTENTIAL).
TNRR-CYS.
BY SIMILARITY.
MISSING (IN ISOFORM 2).
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    Qian F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 572; DB 1; Pred. No. 8.7e-47;
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                                                                                                                                                                                                   BR3
                                                                                                                                 Sciurognathi;
                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                PRT;
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    Vora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
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                                                                                                                                   Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
    Scott M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          III MEMBRANE
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) and 2; are
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                                                                                                                                   Murinae;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Levis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lavis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima M., Mazzarelli J., Mombaerts P.,
A A Kandoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
A Wunshaw-Roris A. Yoshida K. Hascawa Y. Kawaii H. Kohtenki S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cachero T.G., nesuc
                                                                                                                                                                                                                                                                            Promotes the survival of mature B-cells and the B-cell response.

Promotes the survival of mature B-cells and the B-cell response.

Promotes the survival of mature B-cells and the B-cell response.

Promotes the survival of mature B-cells and the B-cell response.

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

TISSUE SPECIFICITY: Highly expressed in spleen and testis; detected at lower levels in lung and thymus.

POISEASE: Defects in TWNFRSF13C are a cause of severe B-cell deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion in the BAFFR gene leading to an altered C-terminus. The mutant RNA is not detectable. B-cell lymphopoiesis is normal, but the life span of peripheral B-cells is much reduced.

FIGURE 13. THE SECONTAINS 1 TWFR-CYS REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-C57BL/6J; TISSUE-Small int
MEDLINE-21085660; PubMed-11217851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yan M., Brady J.K., Chan L., Tank Y.M.;
Cancro M.P., Grewal I.S., Dixit V.M.;
"Identification of a novel receptor for B lymphocyte stimulator that
"Identification of a novel receptor for B lymphocyte stimulator that
"Identification of a novel receptor for B lymphocyte stimulator that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "BAFF-R, a newly with BAFF.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strauch K.,
Ambrose C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Competition for BLyS-mediated signaling peripheral Blymphocyte numbers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wynshaw-Boris A., Yoshida K.,
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harless S.M., Lentz V.M., Sah A.P.,
Hilbert D.M., Hayes C.E., Cancro M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21614654; PubMed=11747827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21475520; PubMed=11591325;
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                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. 11:1986-1989(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNF
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Р.
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                                                                                                                                                                                                                                                                                                                                                                          kb insertion
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There are no restrictions

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EMBL; AK008142; B MGD; MGI:1919299;

Signal-anchor;

Transmembrane; Glycoprotein;

EMBL; AF373847; AAK91827.1; ...

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                                                                                                                                                                                                                                                                                        YOO J., Stone R.T., Beattle C.W.;

YOO J., Stone R.T., Beattle C.W.;

**Cloning and characterization of the bovine Fas.";

DNA Cell Biol. 15:227-234(1996).

-i- FUNCTION: Receptor for TWRSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, on the antigen-stimulated suicide of mature T-cells, on the content of the content of
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REPEAT
          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 6
Teceptor) (Apoptosis-mediating surface antigen FAS)
                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNR6_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFRSF6 OR APT1 OR FAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match
                                                                                                                                                                         both (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
SIMILARITY: CONTAINS 3 TMFR-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                     s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQRYCNASVINSVK---GINAIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLILALTLYGLYSLYSWRWRQQLRTASPDTSEGVQQE-----SLENVFVPSSET--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
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CYTOPLASMIC (POTENTIAL).

THER CYS (PARTIAL).

BY SIMILARITY.

BY SIMILARITY.
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MISSING (IN ISOFORM
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Pred. No. 0.
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(TYPE III MEMBRANE
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Best Local
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Pfam; PF00031; death; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
SMART; SM00208; TNFR, NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1
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CARBOHYD
CARBOHYD
                                                                                      15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
Tumor necrosis fact
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Q96RJ3;
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REPEAT
DOMAIN
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DOMAIN
                 Mammalia; Eutheria;
NCBI_TaxID=9606;
                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                    HUMAN
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 SEQUENCE FROM
                                                 Homo sapiens
                                                            TNFRSF13C
                                                                               activating
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InterPro; IPR001368; TNFR_c
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                                                                                                                                                                                           IMH----
                                                                                                                                                                                                       CIKSKPKVDSDHCFPLPAMEEGATILVT----TKTNDYC---KSLPAALS
                                                                                                                                                                                                                                                                         PCTTCEHGIIEKCTPTSNTKCKGSRSHANSLWAL----LILLIPIVLIIYKVVKSRERNK
                                                                                                                                                                                                                                 KNDYCNSAASNDEGRQLNLTDVDLGKYIPSIAEQMRITEVKEFVRKNGM---
                                                                                                                                                                                                                                                    KDEFKNTGSG-----LLGMANIDL-----EKSRTGD--EIILPRGLEYTVEECTCED
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P25445; 1DDF
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                                                           BAFFR OR
                                                 (Human)
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                                                                         el. 41, Created)
el. 41, Last sequence update)
el. 41, Last annotation update)
el. 41, Last annotation update)
factor receptor superfamily member 13C (B cell-
factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor
                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
 (ISOFORMS 1 AND
                           Chordata;
Primates;
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22.1%;
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(YTOPLASMIC (POTENTIAL).
TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                      DEATH.
BY SIMILAN
                                                                                                                                                                                                                                                                                                                                                               Score 94; DB 1
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUPERFAMILY MEMBER 6. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
TUMOR NECROSIS
                             Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                         Y SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                              4D88A90E9E1F4892
                                                                                                                                                                                                                                                                                                                                                       Mismatches
2)
                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC. .
                                                                                                                                          ⋛
                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                   --RCSSN---
                                                                                                                                                                                                                                                                                                                                                                        Length 323;
                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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Best Local s
Matches 48
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SUBCELLULAR LOCATION: Type III membrane protein (Probable).

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.

TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and in resting B-cells. Detected at lower levels in activated B-cells resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
                                                                                                                                                                                                                                                                                             REPEAT
DISULFID
DISULFID
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Employment on its the European Bioinformatics in the Earn no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thompson J.S., Bixler S.A., Qian F., Cachero T.G., Hession C., Schneider P Strauch K., Zafari M., Benjamin C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is mutated in a mouse strain with severe Curr. Biol. 11:1547-1552(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF373846; AAFGenew; HGNC:17755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-B-cell lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a novel receptor for B lymphocyte stimulator is mutated in a mouse strain with severe B cell deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancro M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yan M., Brady J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21475520; PubMed=11591325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *BAFF-R, a newly identified TNF receptor that specifically interacts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ambrose C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE 21442025; PubMed = 11509692;
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00652; PROSITE; PS50050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 606269;
                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                               Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
                          161
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T 178
                          T 161
                                                                                                                                        W---TCLGLSLIISLAVFVLMF------LLRKISSEPLKDEFKNTGSGLLGMANIDLEKS
                                                                                                                                                                    CVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGLL 78
                                                                                                                                                                                               CSQNEYFDSLLHACIPCQL------RCSSNTP--PLTCQRYCNASVTNSVKGTNAIL 56
                                                      ---DKVII--
                                                                                 RTGDEIILPRGLEYTVEECTC-----
                                                                                                          FGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293:2108-2111(2001).
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00652;
                                                                                                                                                                                                                                                                                                                                                                                                                             Immune response;
                                                                                                                                                                                                                                                                                  100
18
19
24
143
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                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grewal I.S., Dixit V.M.;
                                                      -LSPGISDATAPAWPPPGEDPGTTPP----GHSVPVPATELGSTELVTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK91826.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           TNFR_NGFR_1; FALSE_NEG.
TNFR_NGFR_2; FALSE_NEG.
response; Signal-anchor;
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                                                                                                                                                                                                                                                                                               184
35
32
32
143
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                                                                                                                                                                                                                                                                                    18863
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                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
SIGNAL-ANCHOR (TYPE III MI
(POTENTIAL).
(POTENTIAL).
CYTOPLASMIC (POTENTIAL).
TNER-CYS (PARTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                         Score 93; DB
Pred. No. 0.08
0; Mismatches
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                                                                                                                                                                                                                                                                                  -> PA (IN ISOFORM 2). F2BFB98099A27138 CRC64;
                                                                               EDCIKSKPKVDSDHCFPLPAMEEGATILVTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r'P., Sin
                                                                                                                                                                                                                                       No. 0.088;
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P., Sizing I.D., Mullen C.,
, Tschopp J., Browning J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                     Length 184;
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THE RESULT OF THE PROPERTY OF 
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CONFLICT
CONFLICT
CONFLICT
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CARBOHYD
CARBOHYD
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054990; 035408;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence up
16-0CT-2001 (Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miraglia S., Godfrey
Submitted (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prominin precursor
                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLEEN.
SIMILARITY: BELONGS TO THE PROMININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:1100886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF026269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa;
                                                                                                                                            (Mouse)
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   Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buck D.;
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N-LINKED...
N-> N (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homolog).
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Best Local
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein tyrosine kinase 2 beta (EC 2.7.1.112)
2) (FADK 2) (Proline-rich tyrosine kinase 2) (
beta) (CAK beta) (Calcium-dependent tyrosine )
adhesion focal tyrosine kinase).
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Avraham S., London R., Fu Y., Ota S., Hiregowdar Pasztor L.M., White R.A., Groopman J.E., Avraham "Identification and characterization of a novel tyrostne kinase (RAFTK) from megakaryocytes and J. Biol. Chem. 270:27742-27751(1995).
                                                                                                                                                                                                                                                       Benzing T., Gerke P., Hoepker K., Hildebrandt F., "Nephrocystin Interacts with Pyk2, p130(Cas), and phosphorylation of Pyk2.", proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
                                                                                                                                                                                                                                                                                                             MEDLINE=21396557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adhesion focal tyrosine kinase
PTK2B OR FAK2 OR PYK2 OR RAFTK
                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION OF TYR-402, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96070905; PubMed-7499242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                  FUNCTION: Involved in calclum induced regulation of ion channel and activation of the map kinase signaling pathway. May represent an important signaling intermediate between neuropeptide activated receptors or neurotransmitters that increase calcium flux and the downstream signals that regulate neuronal activity. Interacts with the SH2 domain of Grb2. May phosphorylate the voltage-gated potassium channel protein Kv1.2. Its activation is highly correlated with the stimulation of c-Jun N-terminal kinase activity (By similarity).

CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (Mouse).
 tyrosine phosphate.

SUBUNIT: Interacts with Crk-associated substrate (Cas),
Nephrocystin and GTPase regulator associated with FAK (Graf).

SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocyst
Induces the membrane-association of the kinase.

PTM: Phosphorylated on tyrosines in response to various stim
that elevate the intracellular calcium concentration, as well
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFVANQQTRTRIKGTQK------LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQDAATQLNTNLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----DCIKS-----KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
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867 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                  PubMed=11493697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                844
97112 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86.5; DI
Pred. No. 1.9;
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; F
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> D (IN REF. 2)
D442F6372552B3C8
                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH NEPHROCYSTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1009
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                                                                                                                                                                                                                                                                                                                                                                                                        Avraham H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) (Focal adhesion kinase
(Cell adhesion kinase
kinase) (CADTK) (Related
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                                                                                                                                                                                                                                                                                                                                                                           related brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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                                                                                                                                                                                                                                                                                    Kim E., Walz G.;
tensin and trigg
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; Murinae; Mus
                                           Nephrocystin
                                                                                                                                                                                                                                                                                                                                                                                          adhesion
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                stimuli
                                                                                                                                                                                                                                                                                 triggers
                                                                                                                                                                                                                                                                                                                                                                                                                    Jiang
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Best Local S
Matches 29
    TISSUE-Liver epithelium;

TISSUE-Liver epithelium;

MEDLINE-97094711; PubMed-8939945;

Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.

Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.

Wilm M., Anderegg R.J., Graves L.M., Earp H.S.;

"Activation of a novel calcium-dependent protein-tyrosine kinase."

"Activation with c-Jun N-terminal kinase but not mitogen-activated Correlation with c-Jun N-terminal kinase but not mitogen-activated
                                                                                                                                                                                                                    P70600: Q63201; O8B4B9:
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein tyrosine kinase 2 beta (EC 2.7.1.112)
2) (FADK 2) (Proline-rich tyrosine kinase 2)
beta) (CAK beta) (Calcium-dependent tyrosine FFK2B OR FAK2 OR PYK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
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DOMAIN
DOMAIN
DOMAIN
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protein kinase activation.";
J. Biol. Chem. 271:29993-29998(1996)
                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000001; Euk_pkinase; SMART; SM00295; B41; 1. SMART; SM00219; TyrKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                   SEQUENCE FROM N.A. 672-687 AND 989-998
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PROSITE; PS50011;
PROSITE; PS00109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00109; TYRKINASE. ProDom; PD000001; Euk_pkina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; pkinase; Pfam; PF03623; Focal_AT;
                                                                                                                                                               NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                             FAK2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine-protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:104908;
                                                                                                                                                                                                                                                                                                                                                                                                                      306
                                                                                                                                                                                                                                                                                                                                                                                                                                                 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by PKC activation. Recruitment by Nephrocystin to cell matrix adhesions initiates Tyr-402 phosphorylation. In monocytes, adherence to substrata is required for tyrosine phosphorylation and kinase activation. Anglotensin II, thapsigargin and L-alphalysophosphatidic acid (LPA) also induce autophosphorylation and increase kinase activity (By similarity). SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCLAEFKQI 305
                                                                                                                                                                                                                                                                                                                                                                                                                    RSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
29; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3631; Inc.
:104908; Ptk2b.
:1 PR000719; Euk_pkinase.

5; IPR005189; Focal_AT.

6; IPR001245; Tyr_pkinase.

7770. pkinase; 1
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431
457
549
701
831
868
402
579
1009
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PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              683
439
457
549
767
869
1009
402
579
                                                                                                                                  (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%;
26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                 1),
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PRO-RICH.
FOCAL ADHESION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (AUTO-) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                             Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN
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                                                                                                                                  AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                             1009
                                                                                                                                  SEQUENCE
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SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TARGETING
                                                                                                                                                                                                                                     ) (Focal adhesion kinase (Cell adhesion kinase kinase) (CADTK).
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Length 1009

(FAT).

SIMILARITY).

Phosphorylation.

Indels

32;

Gaps

4

-YCK

166

353

310-334;

Euteleostomi;
Murinae; Rat

Rattus.

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entities
or send a
                                                                                                                                                                                                                                                                                                                                                                            This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBUNIT: ISOSCIATA; but not isoform 2, interacts with Crk-
associated substrate (Cas), Nephrocystin and GTPase regulator
associated with FAK (Graf).
-:- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
induces the membrane-association of the kinase (By similarity).
Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3.
-:- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/PRNK and
3/PYK2s; are produced by alternative splicing.
-:- TISSUE SPECIFICITY: Isoform 1 is expressed at high levels in the
brain (hippocampus, cerebral cortex and oliactory bulb) and poorly
in the spleen and other tissues, whereas isoforms 2 and 3 are
expressed in the spleen and brain (highest in cerebellum).
-- PTM: PDSsphorylated on tyrosines in response to various stimuli
that elevate the intracellular calcium concentration, as well as
by PKC activation. Recruitment by Nephrocystin to cell matrix
adhesions initiates Tyr-402 phosphorylation (By similarity). In
monocytes, adherence to substrata is required for tyrosine
phosphorylation and kinase activation. Angiotensin II,
thapsigargin and L-alpha-lysophosphatidic acid (LPA) also induce
autophosphorylation and increase kinase activity.
-- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINB-95403356; PubMed-7673154; MEDLINB-95403356; PubMed-7673154; Sasaki H., Kotani K., Sasaki T., Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T., "Cloning and characterization of cell adhesion kinase beta, a nove protein-tyrosine kinase of the focal adhesion kinase subfamily."; J. Biol. Chem. 270:21206-21219(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Cell Sci. 111:1981-1991(1998).
                                                                  Pfam; PF00069; Pkinase; 1.
Pfam; PF03623; Focal_AT; 1.
ProDom; PD000001; Euk_Pkina
                                                                                                                                                                                                                                                                                                                     modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                               SMART; SM00295; B41; 1.
SMART; SM00219; TyrKc; 1
                                                                                                                                                InterPro; IPR000719; InterPro; IPR005189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression and characterization of splice variants of PYK2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xiong W.-C., Macklem M., Parsons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98311659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                 InterPro; IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Involved in calcium induced regulation of ion channel and activation of the map kinase signaling pathway. May represent an important signaling intermediate between neuropeptide activated
                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
SUBUNIT: Isoform 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptors or neurotransmitters that increase calcium flux and downstream signals that regulate neuronal activity. Interacts the SH2 domain of Grb2. May phosphorylate the voltage-gated potassium channel protein Kvl.2. Its activation is highly correlated with the stimulation of c-Jun N-terminal kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity
                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                           U69109; AAC52895.1; -. D45854; BAA08290.1; -.
                                                                                                                                                                                        P00523; 2PTK.
                                                                                                                                                                                                       AF063890; AAC28340.1;
                                                                                                                                                                                                                                                                                    an
                                                                      PD000001; Euk_pkinase;
PS00107; PROTEIN_KINASE_ATP; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                   requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase-related protein.";
                                                                                                                                                                                                                                                                                  equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORMS 2 AND 3),
                                                                                                             Tyr_pkinase se; 1.
                                                                                                                                                Euk_pkinase
Focal_AT.
                                                                                                                                                                                                                                                                                                                 is not removed.
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                                                                                                                                                                                                                                                                                                                                   There are no rest
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                                                                                                                                                                                                                                                                                                                       Usage
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  RESULT 9
FAK2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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CONFLICT
CONFLICT
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VARSPLIC
VARSPLIC
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BINDING
ACT_SITE
                                                                                                 MEDLINE=96435932; PubMed=8838818;
Herzog H., Nicholl J., Hort Y.J.,
"Molecular cloning and assignment
adhesion kinase, to 8pil.2-p22 by
Genomics 32:484-486(1996).
                                                                                                                                                                                                         Lev S., Moreno H., Martinez R., Canoll P., Plowman G.D., Rudy B., Schlessinger J.; "Protein tyrosine kinase PYK2 involved in of ion channel and MAP kinase functions."; Nature 376:737-745(1995).
                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).

Homo sapiens (Human).

Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                        TISSUE-Hippocampus; MEDLINE-96435932; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
"Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sas:
"Cloning and characterization of cell adhesion kinase beta,
protein-tyrosine kinase of the focal adhesion kinase subfam
J. Biol. Chem. 270:21206-21219(1995).
                                                   MEDLINE-95403356; F
                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                        MEDLINE=95379967; PubMed=7544443;
                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSIRCLPLEETQAYLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSDHCFPLPAME-----EGATILVTTKTND-----
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                                                                            FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCLAEFKQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase;
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(inase; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  767
869
1009
402
579
771
780
780
205
                                                   PubMed=7673154;
                                                                                                                                                                                                                                                                                                                                        Primates;
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26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO-RICH.

PROCAL ADHESION TARGETING (FAT).

PHOSPHORYLATION (BY SIMILARITY).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

MISSING (IN ISOFORM 2).

NVFKRHSMR -> MGLIVLSSQ (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 82;
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> A (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D435A475BCA49E9B CRC64;
                                                                                                                 , Sutherland G.R. t of FAK2, a nove y nonisotopic in :
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    ATP-binding;

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                                                                                                                                                                                                                                  Ca(2+)-induced regulation
                                                                                                                                                                                                                                                                                                                                        Hominidae;
                                                                                                                                                                                                                                                            Peles
                                                                                                                              G.R.,
                                                                                                                                                                                                                                                                                                                                                                                                      ) (Focal adhesion kinase (Cell adhesion kinase kinase) (CADTK) (Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1009
                                                                                                                                                                                                                                                            [7]
                                                                                                                 situ hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -YCK 166
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human
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                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                            Musacchio J.M.,
                                                                                                                                                                                                                                                                                                                                         Ношо
                                       Sasaki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                           a novel
                                                                                                                                                                                                                                                                                                                                                                                                       (Related
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This SWI
between
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EMBL;
EMBL;
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Pasztor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE Monocytes;
MEDLINE 98211954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasztor L.M., White R.A., Groopman J.E., Avraham H.; "Identification and characterization of a novel related tyrosine kinase (RAFTK) from megakaryocytes and brain."; J. Biol. Chem. 270:27742-27751(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-96070905; PubMed-7499242;
Avraham S., London R., Fu Y., Ota S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monocytes. Activation by a two-stage process involving subsequent intracellular signal.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [4]
SEQUENCE FROM
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                                                                                                                                                                                                              the
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                                                                                                                   send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X., Hunter D., Morris J., Haskill calcium-dependent tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyrosine phosphate.

SUBUNIT: Interacts with Crk-associated substrate (Cas),
Nephrocystin and GTPase regulator associated with FAK (Graf).

SUBCELULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin induces the membrane-association of the kinase.

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

TISSUE SPECIFICITY: Most abundant in the brain, with highest levels in amygdala and hippocampus. Low levels in kidney. Also
                                                                                                                                                                                                                                                                                                                             expressed in spleen and lymphocytes.

PTM: Phosphorylated on tyrosines in response to various stimuli that elevate the intracellular calcium concentration, as well as by PKC activation. Recruitment by Nephrocystin to cell matrix adhesions initiates Tyr-402 phosphorylation. In monocytes, adherence to substrata is required for tyrosine phosphorylation and kinase activation. Anglotensin II, thapsigargin and L-alphalysophosphatidic acid (LPA) also induce autophosphorylation and locrease kinase activity (By similarity).

SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                downstream signals that regulate neuronal activity. Interacts the SH2 domain of Grb2. May phosphorylate the voltage-gated potassium channel protein Kv1.2. Its activation is highly correlated with the stimulation of c-Jun N-terminal kinase activity.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                            increase kinase act: SIMILARITY: BELONGS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natl Acad. Sci. U.S.A. 98:9784-9789(2001).
FUNCTION: Involved in calcium induced regulation of ion channel and activation of the map kinase signaling pathway. May represent an important signaling intermediate between neuropeptide activated receptors or neurotransmitters that increase calcium flux and the
; U33284; AAC50203.1;
; L49207; AAB47217.1;
; D45853; BAA08289.1;
; U43522; AAC05330;1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEPHROCYSTIN.
                                                                                                                   an email to
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, Schilhabel
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                                                                                                                   license@isb-sib.ch).
                                                                                                                                            license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Baumgart C., Dette M.D., Ja
Wen G., Taudien S., Rosentha
EMBL/GenBank/DDBJ databases
                                                                                                                                    agreement (See http://www.isb-sib
                                                                                                                                                               is not removed.
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Rosenthal /
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for
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| triggers
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RESULT 10
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Best Local S
Matches 25
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
     TISSUE-B-cell;
MEDLINE-97458245; PubMed-9311921;
von Buelow G.-U., Bram R.J.;
"NF-AT activation induced by a CAML-interacting necrosis factor receptor superfamily.";
Science 278:138-141(1997).
                                                                                                                              Tumor necrosis factor receptor activator and CAML interactor) TNFRSF13B OR TACI.
                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                        014836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00295; B41; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; pkinase; Pfam; PF03623; Focal_AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S80542; AAB35701.1;
EMBL; AF311103; -; NOT_AN
HSSP; P08631; lAD5.
                                                                                          NCBI_TaxID-9606
                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyrosine-protein
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PROSITE; PS50011;
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                                                                         SEQUENCE
                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000719;
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                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                3X_HUMAN
                                                                                                                                                                                                                                                               DSDHCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                                                                     EFKNTGSGLLGMANIDLEKSR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601212;
                                                                                                                                                                                                                                              RSIRCLPL ---
                                                                                                                                                                                                                                                                                  KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
                                                                       FROM
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                            23
256
435
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256
435
780
780
                                                                                                                                                factor receptor superfamily member 13B
                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                              EEGQAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN_KINASE_DOM;
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                                                                                                                                                                                                                                                                                                                              8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyr_pkinase
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Focal_AT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase;
                                                                                                                                                                                                                                                                                                                                                        NEPHROCYSTIN.

A -> G (IN REF. 3).
G -> P (IN REF. 2).
F -> L (IN REF. 3).
R -> G (IN REF. 2).
A MW; 420B21046274E7C2 CRC64;
                                                                                                                                                                                                                                                                                                               Score 79.5; L. Pred. No. 10; 9; Mismatches
                                                                                                                                                                                                                                                                                                                      9:
                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
MISSING (IN ISOFORM 2).
P->A: LOSS OF INTERACTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO-RICH.
FOCAL ADHESION TARGETING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP
BY S
                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION.
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SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KINASE
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                                                                                                                                                                                                                                                                                                                                       BG
                                                                                                   Hominidae; Homo
                                                                                                                                                                                                                                                                                                                     29;
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                                   member of the
                                                                                                                                                                                                                                                                                                                                       Length 1009;
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                                                                                                             Euteleostomi,
                                                                                                                                                  (Transmembrane
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-!- FUNCTION: Receptor for TWESF13/APRIL and TNESF13B/TALL1/BAFF/BLYS
that binds both ligands with similar high affinity. Mediates
calcineurin-dependent activation of NF-AT, as well as activation
of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
cell function and the regulation of humoral immunity.

-!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
domain of CAMIG with its C-terminus.
-!- SUBCELLULAR LOCATION: Type III membrane protein.
-!- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
intestine and peripheral blood leukocytes. Expressed in resting B-
cells and activated T-cells, but not in resting T-cells.
-!- SIMILARITY: CONTAINS 2 TNER-CYS REPEATS.
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DISULFID
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Tumor necrosis factor (TNF) receptor superfamily member TACI i high affinity receptor for TNF family members APRIL and BLyS."; J. Blol. Chem. 275:35478-35485(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P.,
Garcia A.D., Gollatz E., Dinke D., Lai
Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.
Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
                                                                                                                                                                                                                                                                                                                       DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             humoral immunity.";
Nat. Immunol. 1:252-256(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YU G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
"APRIL and TALL-I and receptors BCMA and TACI: system for regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21170294; PubMed-10973284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20519647;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
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                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ween the Swass instruction. There are no result by non-profit institutions as long as its content is not removed. Usage by are instituted and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.

CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF023614; AAC51790.1; -. BC028072; AAH28072.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:18153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001368; TNFR_c6
                                                                                          187
33
70
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54
71
89
93
128
251
  Conservative
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                                                                              293
104
47
47
62
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66
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1104
1128
251
31816
                                                                                                                                                                                                                                                                                                                                                                                                                                                             response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR_NGFR_1; 1.
TNFR_NGFR_2; FALSE_NEG.
response; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10956646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFRSF13B
                                                                                                                                                                                                                                                                                                                                                                                          165
                   8.1%;
19.9%;
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  35,
                                                                                      N-LINKED (GLCNAC.
P -> L (IN REF. 2);
411799F3DE17A5EB
                                                                                                                                                         TNER-CYS
BY SIMILA
                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
                     Pred.
                                           Score 78.5;
                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR
SIGNAL-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL
                                                                                                                                                         Y SIMILARITY.
  Mismatches
                   No.
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  73;
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                                             Length 293;
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                                       TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                         EMBL; U67575; HSSP; Q54397; TIGR; MJ1357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D., Sutton G.G., Blake J.A., FitzScall L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Weidman J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Francockit, M.D., Roberts R.M., Raine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Francockit, M.D., Roberts R.M., Raine B.P., Borodovsky M., Romacchit, M.D., Roberts R.M., Raine B.P., Borodovsky M., Raine B.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YD57_METJA
Q58752;
                                                                                                                                                                                                         InterPro; IPR001622; K+channel_pore
InterPro; IPR000309; TrkA_Kuptake.
InterPro; IPR003148; TrkA_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative potassium channel MJ1357.
                                                                                                          TRANSMEM
                                                                                                                                             Hypothetical
                                                                                                                                                                      Pfam; PF02080; TrkA-C; Pfam; PF02254; TrkA-N;
                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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(Rel. 35, Last sequence up)
(Rel. 40, Last annotation
                                                                                                                                             protein;
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                                                                                                                                                Transmembrane; Transport;
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Score 78.5;
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61231B0C001B54C4
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                                            CRC64;
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Length 343;
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RX STRAINCESTRIFE, FAUTH IN. A.

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RA ARAWAN T., HARA A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Alzawa T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Kadota K., Matsudo H.A., Ashburner M., Batalov S., Casavant T., RA Kadota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchionni L., Mashina J., Mazazarelii J., Mombaerts P., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 13B
activator and CAML interactor).
TNFRSF13B OR TACI.
Mus musculus (Mouse).
Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Spleen;
MEDLINE-21177254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalla; Eutheria;
NCBI_TaxID=10090;
                                                                                                      Hayashizaki Y.; Functional annotation of Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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15-JUN-2002
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S.A., Grewal I.S.,
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Rodentia;
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249
                                                                                                                        mouse
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Best Local
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"TACI is a TRAF-interacting receptor for TALL-1, a factor family member involved in B cell regulation.
J. Exp. Med. 192:137-143(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
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CONFLICT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institutions as long as its content is in the content in the content in the content is in the content in the content in the content is in the content in th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen-induced arthritis in mice.";
Nat. Immunol. 2:632-637(2001).
-i- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS that binds both ligands with similar high affinity. Mediates
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21322748; PubMed=11429548; Wang H., Marsters S.A., Baker T., Chan B., Lee Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.; "TACI-ligand interactions are required for T ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                        143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMIG with its C-terminus (By similarity). SUBCELLULAR LOCATION: Type III membrane protein (Probable). SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBUNIT: Bin
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ITE; PS00652;
                                                                                                                                                                                                                                                                                      QNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCN---ASVTN------SVKGTN
                                      CF----PLPAMEEGATI
                                                                               PRGSQANSPHAHRPVTEACDEVTASPQPVE---
                                                                                                                                                                                                                                                 QGRYYDHLLGACVSCDSTCTQH---PQQCAHFCEKRPRSQANLQPELGRPQAGEVEVRSDN
                                                                                                                      TGSGLLGMANIDLEKSRTGDEIIL-PRGLEYTVEECTCEDCI-----KSKPKVDSDH
                                                                                                                                                               SGRHQGSEHGPGLRLSSDQLTLYCTLGVCLCAIFCCFLVALASFLRRR--GEPLPSQPAG
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                                                                                                                                                                                                                                                                                                                                 l Similarity
43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50050; TNFR_NGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immune
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TNFR_NGFR_1;
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149
                                                                                                                                                                                                    ----ILWTCLGLSLIISLAVFVL---MFLLRKISSEPLKDEFKN
                                                                                                                                                                                                                                                                                                                                                    8.0%;
21.7%;
                                      155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POT TNER-CYS 1.
TNER-CYS 2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                  Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -y....-unchor; Transmembrane; Repeat.
EXYRACELLULAR (POTENTIAL).
SIGNAL-ANCHOR (TYPE III MEMBRANE PRO
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                   CB2F2D61C2931D81 CRC64;
                                                                                                                                                                                                                                                                                                                               Mismatches
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3.9;
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RESULT 13
YCSB_SCHPO
                                                                                                                                    A FEDERAL REPRESENTATION OF THE PROPERTY OF TH
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders S., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders S., Seeger K., Whitehead S.,
RA Faylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vonstreels E., Rieger M., Scheefer M., Wheller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Scheefer M., Mueller-Auer S.,
RA Gobel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gel Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RT "The genome sequence of Schizosaccharomyces pombe.";
   Query Match
Best Local S
Matches 44
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical WD-repeat protein C613.12c in chromosome
SPCC613.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCSB_SCHPO
074910;
                                                                                                                                                                                          PROSITE; PS00678; WD_REPEATS_1; 2.
PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE: PS50094; WD_REPEATS_REGION; 1.
Hypothetical protein; Repeat; WD repeat
REPEAT 297 336 WD 1.
REPEAT 486 525 WD 2.
REPEAT 486 528 WD 3.
REPEAT 544 583 WD 3.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00320; GPR07
SMART; SM00320; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL031644; CAA21064.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21848401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                 Similarity
                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPROTEINBRPT
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                                                                                                                             525
583
626
71536
                           7.8%;
22.7%;
                                                                                                                                    X.
      20;
                                                                                                                                                            WD 1.
WD 2.
WD 3.
WD 4.
                                 Score 75.5;
Pred. No. 1:
                                                                                                                                6CD360D8748AAF98 CRC64;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638
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                                                                DB 1;
   61;
                                                                Length 638;
   Indels
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   69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thode G.,
   Gaps
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7;
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Pfam; Pfam; Pfam;

PF00069; PF00954; PF01453;

pkinase; 1.
S_locus_glycop; 1.
Agglutinin; 1.

InterPro; IPR002290; InterPro; IPR000858;

InterPro; IPR001480; InterPro; IPR000719;

Euk_pkinase B_lectin

IPR003609; IPR004040;

STY_pkinase. Ser_thr_pkin Pan_app.

Slocus_glycop

the

between

or send

s requires a license agreement (an email to license@isb-sib.ch)

(See http://www.isb-sib.ch/announce/

EMBL;

M76647; AAA33000.1; ALT_TERM

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STRAIN-CV. S6S6; TISSUE-Stigma;

MEDLINE-92020942; PubMed-1681543;

Stein J.C., Howlett B., Boyes D.C., Nasrallah M.E.;

**Molecular cloning of a putative receptor protein kinase ge at the self incompatibility locus of Brassica oleracea.**;

Proc. Natl. Acad. Sci. U.S.A. 88:8816-8820(1991).

-i- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION), PROBABLY ACTING IN COMBINATION WITH S-L SPECIFIC GLYCOPROTEINS. INVERFACTION WITH A LIGAND IN THE STREET COMBINATION WITH S-L SPECIFIC GLYCOPROTEINS. INVERFACTION WITH A LIGAND IN THE STREET COMBINATION WITH S-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-KDV-1995 (Rel. 32, Last annotation update)
Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q09092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea (Cauliflower).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (S-receptor
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                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY IN THE PISTIL AND ANTHER.
POLYMORPHISM: THERE ARE A NUMBER OF DIFFERENT S ALLELES IN
B. OLERACEA, POSSIBLY PROVIDING THE RECOGNITION SPECIFICITY.
SIMILARITY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS
GLYCOPROTEINS OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN IS
A SER/THR-PROTEIN KINASE RELATED TO RAF KINASES.
                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on the by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR DOMAIN TRIGGERS THE PROTEIN KI CYTOPLASMIC DOMAIN.
CATALYTIC ACTIVITY: ATP + a protein - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRAOL
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Best Local s
Matches 33
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P41771;
01-NOV-1995
01-NOV-1995
01-NOV-1995
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SIGNAL
1 32 POTENTIAL.
CHAIN 33 849 PUTATIVE CEPTUM TO THE CEPTUM T
                                                                                                                                                                            Dean N.; "Cloning and DNA sequence of a Kluyveromyces lactis Yeast 10:1117-1124(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLULA
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PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-95084639; PubMed-7992512;
                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota;
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                                                                                                      FUNCTION: REQUIRED FOR THE RETENTION OF LUMINAL E RETICULUM PROTEINS, AFFECTS GLYCOPROTEIN PROCESSI
                                 GOLGI APPARATUS.
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWT-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADIAKKRNASGKIISLTVGVSVLLLLIMFCL-----WKRKQKRAKASAISIANTQRNQ
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SM00108; B_lectin; 1.
SM00473; PAN_AP; 1.
SM00221; STYKC; 1.
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17.6%; Pred. No. 23;
Live 30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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O8r056 mus musculu
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O8rwv7 arabidopsis
O9r491 ovis aries
O8vev6 mus musculu
O94/11 paramecium
O39191 arabidopsis
O01892 caenorhabdi
O81820 arabidopsis
O26489 spodoptera
O8vfw0 mus musculu
O9h6/7 homo sapien
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ALIGNMENTS

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112 EIILPRGLEYTVEECTGEDCIKSKPKVDSDHGFPLPAMEBGATILVTTKT 161		57 WTCLGLSLIISLAVFYLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111	21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80	NEYFDSLLHACIP	Query Match 12.1%; Score 116.5; DB 11; Length 175; Best Local Similarity 29.4%; Pred. No. 0.0002; Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8	SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;	EMBL; AF350257; AAL83914.1;	Octiviar F-actin content.";	Identification of novel TRAF3 binding protein, T3BP, which increases	Mizuno K., Irie S., Sato TA.;	SEQUENCE FROM N.A.	[1]		Mammalia: Eutheria: Rodentia: Schurognathi: Muridae: Murinae: Mus.	Carrier Worthhorte	TRAF3 binding protein.	. 21,	(TrEMBLrel. 21,	Vor+ws; 01-JUN-2002 (TrEMBLrel. 21, Created)	Q8R4W8 PRELIMINARY; PRT; 175 AA.	1

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01-OCT-2001 (TrEMBLrel. 18, L
01-DEC-2001 (TrEMBLrel. 19, L
Amino acid ABC transporter, p
CAC3619
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J. Bacteriol. 183:4833-4883 (2001).
EMBL; AE007858; AAK81542.1;
InterPro; IPR000515; BPD_transp.
Pfam; PF00528; BPD_transp; 1.
PROSTIE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
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MEDLINB-21359325; PubMed-11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Tatusov R.L., Sabathe F., Doucette-Stamm L., Souca Bennett G.N., Koonin E.V., Smith D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium acetobutylicum.

Bacteria; Firmicutes; Bacillus/Clostridium group;
Clostridiales; Clostridiaceae; Clostridium.
                                                              Submitted (APR-2002) to the EMBL; BC028286; AAH28286.1; Hypothetical protein. SEQUENCE 842 AA; 94478 MM
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-ATCC 824 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q97D61;
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                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                TISSUE-EYE;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical 94.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8R056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8R056
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                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
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   Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFPLPAMEEGA--TILVTTKTNDYCKSLPAALSATEIEKSIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLLLQLYVYYYGLPFLSDKLTMTPMKAAILGLSLNSGAYIAEIIRGGILAIDNGQFEASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLNKVIPVLLDGTRITLLLTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLLHACIPCQLRCSSNTPPLTCQRYCNASV-----TNSVKGTNAI----LWTCLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TGDEIILPRGLEYTVEEC--------TCEDCI-KSKPKVDSDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteome.
217 AA;
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Rodentia;
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                                                                 MW;
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                                                                                                                                                              EMBL/GenBank/DDBJ
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 88.5;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36738BCDC0DE8A2F CRC64;
                                                                 734C10D715E5BC92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
86.5;
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                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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11;
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Length 842;
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                               ProDom: PD000001; Euk_pkinase;
SMART; SM00261; FU; 6.
SMART; SM00220; S.TKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99246375; PubMed=10229568;
Suga H., Koyanagi M., Hoshiyama D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydatia fluviatilis.
Eukaryota; Metazoa; Porifera
Haplosclerida; Spongillidae;
                               PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                         InterPro; IPR002290; InterPro; IPR001368; InterPro; IPR001245;
                                                                                                                                                                                                                                               parazoan-eumetazoan split.
Gene 280:195-201(2001).
                                                                                                                                                                                                                                                                                           MEDLINE=21601119; PubMed=11738833; Suga H., Katoh K., Miyata T.;
                                                                                                                                                                                                                                                                                                                                     "Extensive gene duplication in the early eventhe parazoan enumetazoan split demonstrated tyrosine kinases from sponge and hydra."; J. Mol. Evol. 48:646-653(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Y1X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9Y1X8
          Kinase
                     PROSITE;
                                                                                                             PRINTS; PRO0109; TYRKINASE.
                                                                                                                          Pfam;
                                                                                                                                               Pfam;
                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                 Suga H., Katoh K., Miyata T.;
"Sponge homologs of vertebrate
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   Miyata T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=31330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein tyrosine kinase
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                                                                                                                       PF00757; Furin-like; 1. PF00069; pkinase; 1. PF01030; Recep_L_domain;
                                                                                                                                                                                                                           P08631;
                                                                                                                                                                                                                                      AB006570; BAA81724.2;
                     PS00652;
                                                                                                                                                                                                       IPR000719;
                                                                                                                                                                                                                 IPR000494;
                                                                                                                                                                                          IPR002174;
1193
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                   TNFR_NGFR_1;
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                                                                                                                                                          Tyr_pkinase.
                                                                                                                                                                    Ser_thr_pkinase
TNFR_c6.
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Last annotation update)
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Ephydatia.
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                      UNKNOWN_1.
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RESULT
Q9STR8
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01-JUN-2002 (TIRMBLrel. 21, Last sequence up
01-JUN-2002 (TIRMBLrel. 21, Last annotation
Hypothetical 103.6 kDa protein.
AT3G48195.
   01-MAY-2000 (
01-MAY-2000 (
01-DEC-2001 (
Hypothetical
T24C20_80.
                                                                                         Q9STR8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M., Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C. J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki Davis R.W., Ecker J.R., Theologis A., "Arabidopsis Full Length cDNA Clones.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein
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                                                                                                                                                                                                                                     EEGAT I
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(TrEMBLrel. 13, Last
(TrEMBLrel. 19, Last
1 223.5 kDa protein.
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22.3%;
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                                                       Created)
Last sequence update)
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Pred. No. 4
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                                     annotation update)
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RESULT
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Best Local Similarity
Matches 37; Conserv
Pfam; PF00531; death; 1.

Pfam; PF00020; TNFR_C6; 3.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 3.

SMART; SM00208; TNFR; 1.

PROSITE; PS500017; DEATH_DOMAIN; 1.

PROSITE; PS00652; TNFR_NGFR_1; 1.

PROSITE; PS00652; TNFR_NGFR_2; 2.

SEQUENCE 327 AA; 36928 MW; 5CFEE
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01-MAY-1999
01-MAY-1999
01-JUN-2001
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
EMBL; AL096856; CAB51067.1;
InterPro; IPR001515; BPD_transp.
InterPro; IPR001683; PX.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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SMART: SM00312; PX; 1.
PROSITE: PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 1998 AA;
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                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pećora; Bovoidea;
Bovidae; Caprinae; Ovis.
NCBI_TaxID-9940;
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                                                                                                                                                                                                                   Submitted (MAR-1998) to the EMBL; AB011671; BAA37093.1;
                                                                                                                                                                                                                                                     Takagi M., Takahashi H., Kabeya H., "Cloning of sheep fas antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries (Sheep).
                                                                                                                                                      InterPro; IPR000488; Death. InterPro; IPR001368; TNFR_c6
                                                                                                                                                                                                  HSSP; P25445; 1DDF
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=LYMPHOCYTE;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
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8; Mismatches
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Pred. No. 11;
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Matches 54
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Best I
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Q94711;
Q1-FEB-1997
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Q1-FEB-1997
Q1-FEC-2001
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Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY073792; AAL61455.1; -. InterPro; IPR000276; GPRC_Rhodpsn. Pfam; pF00001; 7tm_1; 1. Pt. PF0051TE; pS00237; G_PROTEIN_RECEP_F1_1; UNKNOW PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01factory receptor MOR202-38.
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                     51C
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    Paramecium
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                     surface
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olfactory recep
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tetraurelia
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y receptor gen
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.1;
6; Mismatches
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                                                                                                                             PRT;
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Best Local (
                           EMBL; L0399; AAA32844.1;

InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF_L1ke.
InterPro; IPR0001581; EGF_CA.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR000219; Euk_pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00011; EGF_CA; 1.
SMART; SM00011; EGF_CA; 1.
PROSITE; PS01186; EGF_C; UNKNOWN_1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS001187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidonsis.
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MEDLINE-92106337; PubMed-1762150;

Mielsen E., You Y., Forney J.;

"Cysteine residue periodicity is a conserved structural feature

"Cysteine residue periodicity is a conserved structural feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002895; Paramecium_SA. Pfam; PF01508; Paramecium_SA; 25. SEQUENCE 2233 AA; 237078 MW; CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variable surface proteins from Paramecium tetraurelia.";
J. Mol. Biol. 222:835-841(1991).
EMBL; M65164; AAA61740.1; -
                                                                                                                                                                                                                                                                                                                                      Smith T.A., Kohorn B.D.;
"An Arabidopsis serine threonine kinase homologue with selected in yeast for its specificity for a thylakoid r
                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 8
                                                                                                                                                                                                                                                                                                                      protein."
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93066369; PubMed=1438303;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine threonine
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                    ATP-binding;
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   Serine/threonine-protein kinase;
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                 Calcium-binding; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Last sequence update)
Last annotation updat
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7; Mismatches
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Pred. No. 2
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E SER/THR FAMILY OF PROTEIN
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                 Glycoprotein;
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                                                                                                                                                                                                                                                   Waterston
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                         Submitted (JUN-1999) to the EMBL; AF003385; AAB54249.1; HSSP; P05164; 1CXP.
                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R08F11.7
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                         InterPro; IPR002007; Anim_peroxidase.
Pfam; PF03098; An_peroxidase; 1.
SEQUENCE 773 AA; 83992 MW; 4E3373
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itted (MAY-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                                                   PCQLRCSSNTPPLTCQ------RYCN----ASVTNSVKGTNAILWTCL---GLSL 64
SSLNCTSC--SSPTTISTNCAPIPAPADDKYFTPVSRTEARCIRLTRALNGQSGFGVRTQ
                      EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA-----TE
                                                                                           PPKSNATCQGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA
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Pred. No. '
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4E3373FDA4EC67C7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000001; Euk_pkinase; 1.

R SMART; SM000179; EGF_CA; 1.

R SMART; SM000179; EGF_Like; 1.

R SMART; SM00011; EGF_Like; 1.

R PROSITE; PS01186; EGF_2; UNKNOWN_1.

R PROSITE; PS01186; EGF_CA; UNKNOWN_1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01018; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS01018; PROTEIN_KINASE_TOM; 1.
                                                                                                                                                                                                                                                                   Matches
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O81820; O1-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Wall-associated kinase 1 (Putative wall-associated wakl OR F16F4.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M., Quach H.L., Tang C., Toriuni M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
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InterPro; IPR004040; STY_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL; AJ009696; CAA08794.1; -. EMBL; AY009917; AAK64021.1; -. InterPro; IPR000152; ASX.hydroxyl. InterPro; IPR000561; EGF-like. InterPro; IPR001881; EGF-Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sakurai T., Satou M., Seki M., Shinn P., Southwick / Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene F16F4.6 (GI:8920634)."; Submitted (JUN-2001) to the EMBL/GenBank/DDD database s
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"A cluster of five cell wall associated receptor kinase genes, Wakl-5, are expressed in specific organs of Arabidopsis.";
plant Mol. Biol. 39:1189-1196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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InterPro; IPR002290; Ser_thr_pkinase.
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        TNSVK-----GTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL--
                                                                                                                                                                          CSQNEYFDSLLHACIPCO--LRCSSN-----TPPLTCQR-----YCNA-----
                                                                                              CRCNEGFDGNPYLSAGCQDVNECTTSSTIHRHNCSDPKTCRNKVGGFYCKCQSGYRLDTT
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                                                                                                                                                                                                                                                                                                       8.3%;
                                                                                                                                                                                                                                                          27; Mismatches
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Pred. No.
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TMSCKRKEFAWTTILLVTTIGF-LVILLGVACIQQRMKHLKDTKLREQFFEQNGGGMLTQ

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GMANID --

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RESULT Q8VFWQ PDT QC QC QC QC QC RP RP
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                                                           Q8VFW0 PRELIMINARY; PRT; 3:
Q8VFW0;
Q8VFW0;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-7002 (TrEMBLrel. 21, Last seque)
Q1-JUN-2002 (TrEMBLrel. 21, Last annot.
Q1-JUN-2002 (TrEMBLrel. 20, Last seque)
Q1-JUN-2002 (TrEMBLrel. 21, Last seque)
Q1-JUN-2002 (TrEMBLrel. 20, Last seque)
Q1-JU
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Best Local Similarity
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Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
Probom; PD000717; P_domain; 1.
SMARP; SW00261; FU; 10.
SMARP; SW00261; FU; 10.
PROSITE; PS00136; SUBTILASE_HS9; 1
PROSITE; PS00138; SUBTILASE_SER; 1
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Spodoptera frugiperda (Fall armyworm).

Spodoptera frugiperda (Fall armyworm).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;

Eukaryota; Neoptera; Endopterygota; Lepidoptera; Glos

Noctuoldea; Noctuidae; Amphipyrinae; Spodoptera.

NCBI_TaxiD=7108;
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ data EMBL; 268888; CAA93116.1; "...
HSSP; Q99405; 1MPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21,
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InterPro; IPR000209; Peptidase_S8
InterPro; IPR002884; P_domain.
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                                                                Craniata; Vertebrata; Sciurognathi; Muridae;
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SEQUENCE FROM N.A.

Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Sh Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Sh Okitani R., Ota T., Sugano S.;

"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO26184; BAB15387.1;

SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
01-MAR-2001 (TrEMBLrel. 16, Last annotation
CDNA: FLJ22531 fts, clone HRC12890.
Homo sapiens (Human).
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InterPro; IPR000276; GPC_Rhodpsn.
Pfam; PF00001; 7tm.1; 1.

PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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IMGVYTLLTTHLN
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AAB08843
AAY94001
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AAE00506
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165	146	114	50	50	50	50	623	252	161	1174	1165	766	526	526	526	475	456	450	439	401	394	369	369	344	193	166	646	639	294	281	1118	969	542	542
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AAG20000	AAG57044	AAG57045	ABG40174	AAM70525	ABB22692	ABB37396	ABB61371	ABB60972	AAU43223	ABP26712	ABP29975	AAY00870	AAU76341	AAU76340	AAB68985	AAG39947	ABB60009	AAG31130	ABB67383	ABB65832	AAG39948	AAG39949	AAG31131	11	4	12	AAU36711	38	12	12	292	90	432	AAY00040
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ALIGNMENTS

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Human B-cell maturation (BCMA) protein.
                                       12-MAR-2002
                                                                                AAE15484;
                                                                                                                      AAE15484 standard; Protein; 181 AA.
                                       (first entry)
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RESULT 1
AAE15484
IID AAE15484
XX AAE15484
AC AAE1
XX AAE1
XX Huma
DE Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX The Service Avertage Avertag Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNR; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis. WO200187979-A2 Domain Homo sapiens Region /note= "Cysteine-rich consensus region; This is region is specifically claimed as SEQ ID NO: 7 in claim 1 of the specification" 52..72 /label= Transmembrane_domain

ABB81487 AAY00041 ABP43260

Human BCMA recepto Enterococcus faeca E faecalis EF017 a

22-NOV-2001.

Human

cell matur

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RESULT 2
AABO8843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 7
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27-JUN-2000;
14-MAY-2001;
                                                                                                                                                      BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory respreheumatoid arthritis; inflammatory bowel disease; septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                          Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theill
31-AUG-2000
                                                                                                                                                                                                                   Amino acid sequence of human.
                                                                                                                                                                                                                                                                                     AAB08843;
                                                                                                                                                                                                                                                                                                               AAB08843 standard; peptide; 184 AA
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                                                                             Domain
                                                                                                                         Homo
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                             WO200050633-A1
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les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          1 EKSRTGD 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCMA protein.
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; 2000US-214591P.
; 2001US-0214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                  (first entry)
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                                                                         Location/Qualifiers 57..77
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                                                            "putative transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                     response;
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RESULT 3
AAY94001
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
                                                                                                               immune response; immunosuppression; graft rejection; joint | graft versus host disease; inflammation; swelling; anaemia; insulin dependent diabetes mellitus; Crohn's disease; hyperi
                                                                                                                                                               systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
                                                                                                                                                                                                                                  transmembrane activator and CAML-interactor; tumour necrosis factor; ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
                                                                                                                                                                                                                                                                                                       A human BCMA protein, a B cell protein related to TACI.
                                                                                                                                                                                                                                                                                                                                                                                                          AAY94001 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene and
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                                                                                                 renal artery stenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 EKSRTGD
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                                                               sapiens
                                                                                                                                                                                                                                                                     BR43x2; TACI receptor;
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                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that modulate NF-kB expression and thus for drug
                                                                                                   occlusion; cholesterol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
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                                                                                                                                                                                                                                                     extracellular domain; BCMA; B cell protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                 graft rejection; joint pain;
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                                                                                                               hypertension
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RESULT 4
AAE09241
ID AAE0
XX AAE0
AC AAE0
AC APEC
XX 19-N
XX Humma
KW Humma
KW TNFF
KW PSOJ
XX PSOJ
XX WO21
XX WO21
XX PF 28-
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity and BR43x2. TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, emphysema, end stage renal failure, glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal neoplasms, multiple myelonmas, lymphomas, light chain neuropathy, amyloidosis, moderating immune response, inflammation, insulin dependent rejection, graft versus host disease, inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or septic shock BR4dx2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF) receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used for inhibiting Bt43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an authorise and disease solociated for content of the second content of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                            Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
                                                                                                                                                                                                                                                                                                                                                             Human BCMA protein
  28-NOV-2000; 2000WO-US32378.
                                                                                                             WO200160397-A1
                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                     autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                          19-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE09241 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                         23-AUG-2001
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                  rheumatoid arthritis; multiple sclerosis;
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Pred. No.
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5.7;
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06-OCT-1999; 11-FEB-2000; 30-JUN-2000;

2000US-0181807 2000US-0215688

99US-0157933

12-APR-2001 WO200124811-A1

05-OCT-2000;

2000WO-US27579

Homo

tumour necrosis

factor;

BCMA;

B cell maturation

protein

B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF;

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RESULT 5
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APPRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity TALL-1 and APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, and coloning the sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCMA
                                                                                                                                                                                                      Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
                                                                                                                                                                                                                                                                    Human B cell maturation protein (BCMA).
                                                                                                                                                                                                                                                                                               31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                    AAE00506 standard; Protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity, for treating autoimmune disorders and cancer, con exposing the cells to TALL-1 or APRIL polypeptide agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yan
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22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    105 EKSRTGD 111
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)B; AAD15902.
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2000US-0226986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lupus erythematosus. The present sequence is human
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Pred. No.
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                                                                                                                                                                    Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell matureation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoprolliferative disorder; hypertension renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's diseases, systemic lupus erythematosus-SLE); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, immunosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HIV), and for treating, suppressing or altering an immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is human APRIL-R also referred as BCMA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or useful for treating undesired cell proliferation such as cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) antagonist
                16-AUG-2000;
                                                     22-FEB-2001
                                                                                    WO200112812-A2
                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                 Human BAFF receptor (BAFF-R).
                                                                                                                                                                                                                                                                                                                                                                        22-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                         AAB60698;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB60698 standard;
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(APOT~) APOTECH R & D
                                                                                                                                                       Lympnoma; gene
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7; Conser
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ilarity 100.0%;
Conservative (
                  2000WO-US22507
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                                                                                                                                                       therapy; cancer;
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Pred. No. 5.7;
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Human B cell maturation factor (BCMA) protein.

28-MAR-2001 AAY71979;

(first entry)

AAY71979 standard; Protein; 184

0

Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucoyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus; thrombocytopenia purpura; acute rheumatic fever; Goodpasture's Syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;

B cell maturation

factor;

pemphigus vulgaris;

B-lymphocyte proliferation

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Вþ
                                                                                                                                                       the TNF (tumour necrosis factor) family, acting as an immunoregulatory cagent, and also plays a role in the development of hypertension and crelated disorders. BAFF-R, fusion proteins containing it, and BAFF-R-CC specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV cell in the treatment of immunosuppressive disorders and HIV cell in the treatment of immunosuppressive disorders and HIV cell in the treatment of immunosuppressive disorders and HIV cell in the treatment of immunosuppressive disorders and HIV cell in the factor of the superior of treating.

CC suppressing or altering an immune response involving a signalling pathway cell suppressing or altering an immune response involving a signalling pathway cell suppressing the superior in the suseful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, rapidly concerning the superior and lumphoppes where a cell diseases.
                                                                             Matches
                                                                                             Query Match
Best Local
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11-FEB-2000;
18-FEB-2000;
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(APOT-)
                                                                                                                                                                                            present sequence represents human
                                                                                                                                                                                                              human BAFF-R may be used in gene therapy to treat tumours, lymp autoimmune disorders and inherited B-cell-associated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                     progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Fig 1; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody
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105
                                      1 EKSRTGD 7
EKSRTGD
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                                                                        7; Conserv
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APOTECH R & D
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                                                                                                                                                     184 AA;
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2000US-0181684.
2000US-0183536.
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to the use of a
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                                                                                           100.0%;
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                                                                                           Score 36; DB
Pred. No. 5.7;
                                                                        Mismatches
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                                                                                                             Length 184;
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Homo sapiens

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to Tumour necrosis factor (TNF) and ApoL-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful realing B lymphocyte associated autoimmune disorders like rheumatoid arthurs and account of the second actions and the second actions are applied to the second actions and the second actions are actions as a second action of the second actions are actions as a second action of the second actions are actions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarieritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in diagnostic assays.

The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not by brain, muscle, heart, lung, kid pancreas, testis and placenta. BCMA mRNA is absent in the pro-B lymphocyte stage but its expression increases with B lymphocyte
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01-MAY-2000;
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                 Human BCMA receptor related protein SEQ ID NO:7
                                                  02-SEP-2002 (first entry)
                                                                                                                      ABB81487 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                               184 AA;
                                                                                                                                                                                                                                                                             Conservative
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2000US-0201012
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                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                             Score 36;
Pred. No.
                                                                                                                                                                                                                                                                               Mismatches
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5.7;
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                                                                                                                                                                                                                                                                                                             Length 184;
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RESULT 9 AAY00041

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds 2tnfrl2 (e.g. ZTNF4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (I) is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated human tumor necrosis factor receptor polypeptide, t Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease. (I) is useful for modulating the immune system, for regulating B cell responses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                designated Ztnfr12 (1). (1) has cytostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidabetic, antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOY-2000; 2000US-246449P
20-DEC-2000; 2000US-257131P
28-JUN-2001; 2001US-301715P
29-AUG-2001; 2001US-315565P
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                                                                                                                                                                                                                                                                                                                                                                 production and cytokine production, and for modulating T and communication. The present sequence represents a protein whice given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a human tumour necrosis factor receptor designated Ztnfrl2 (1). (1) has cytostatic, immunosuppressive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 135-136; 154pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           development,
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   105
                                                                      EKSRTGD
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06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                            New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
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                                                            E faecalis
                                                                               05-AUG-2002
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   US2002045737-A1
                     Enterococcus
                                      Enterococcus; vaccine;
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DB; AAX20031.
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97US-0046655.
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85.7%;
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                                      gastrointestinal disease; diagnosis; antibiotic
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antigenic.
                                                         fragment
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06-MAY-1997;
16-MAY-1997;
products
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New isolated products for
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The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis infection. The present sequence is a protein of the invention.
                                       WPI; 1999-070095/06
N-PSDB; AAX20030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genes and polypeptides from Enterococcus faecalis, useful vaccines for preventing, treating or attenuating an infection a member of the Enterococcus genus in an animal, particularly faecalis
                                                                                                                                                                                                                                                                                                       detection; attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAY00040 standard;
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Enterococcus faecalis polynucleotides the detection of Enterococcus and for
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                                                                                                              The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis infection. The present sequence is a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                      s and polypeptides from Enterococcus faecalis, useful for preventing, treating or attenuating an infection of the Enterococcus genus in an animal, particularly
                                                                                                                                                                                                                                                                                Page
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                                                                                                                                                                                                                                                                             255pp;
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  . 98;
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                                                                                                  for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of [I]) or to treat disease states involving CC (II). (II) is useful for generating annibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and constraints and sequences. ABG00010-ABG30377 represent novel human acid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO as the product of the invention.
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                                                                                                                                                                                                                                                                                                                                                      polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                      polynucleotides are also used in diagnostics as expressed sequence tags
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DB; AAS93250.
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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                              DB 22;
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                    17-OCT-2000
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form specification, but was obtained in electronic i at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 15567; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic a genes from Drosophila interactions -
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N-PSDB; ABL07028.
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11-JUL-2000; 2000US-0614150.
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                                                                     Score 31; DB 21;
Pred. No. 1e+02;
0; Mismatches
                                                                      1:
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22-JUN-1999
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99US-0142864.
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Perfect score:
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   pred. No. is the score greater than and is derived
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seq length: 2000000000
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
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US-09-361-707-42
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US-08-462-881-7
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US-08-479-895-5
US-08-791-0058-7
US-08-791-0058-7
US-08-791-281-4
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US-09-071-035-64
                                                                 Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                            TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gil H. C)
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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405 EKSRSGD 411
                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 9410 Ke
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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Y: USA
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Sequence L	771-711-818-80-50	4	Ł,	12.2	20	ţ
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Sequence 56,	US-08-818-112-56	4	19	72.2	26	44
Patent No. 516448!	5164485-4	Φ	14	72.2	26	3
Sequence 6, Appl	US-08-762-428A-6	ω	1288	75.0	27	42
Sequence 97,	US-09-232-201-97	4	650	75.0	27	41
Sequence 79,	US-09-232-201-79	4	650	75.0	27	0
Sequence 97	US-09-232-197-97	4	650	75.0	27	39
	US-09-232-197-79	4	650	75.0	27	88
Sequence 97	US-09-232-200-97	4	650	75.0	27	37
	US-09-232-200-79	4	650	75.0	27	36
	US-09-232-191-29	4	650	75.0	27	35
Sequence 75	US-09-232-201-75	4	590	75.0	27	34
	US-09-232-197-75	4	590	75.0	27	33
Sequence 75,	US-09-232-200-75	4	590	75.0	27	32
Sequence 25,	US-09-232-191-25	4.	590	75.0	27	31
Sequence 114, App	US-09-721-362-114	4	476	75.0	27	30
Sequence 6, Appli	US-09-134-218-6	4	476	75.0	27	29
Sequence 114	US-09-315-444-114	4	476	75.0	27	28

ALIGNMENTS

faecalis

Polynucleotides and Polypeptides

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REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.51
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE
                                                                                                               521 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Human Genome Sciences,
9410 Key West Avenue
                                                                                                                                                      309-8512
                                                                                                                                                                                                                                                                                                                                                   MSDOS version
            88.9%;
85.7%;
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                                                                                                                                                                                                     36,373
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Score 32; DB Pred. No. 29; 1; Mismatches
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US-09-071-035-62
                                                                                                                                                                                                                                                                                             US-09-463-238-6
                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                            Sequence 6, Application US/09463238 Patent No. 6469230
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local :
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                                                                  CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
                                                                                                                      APPLICANT: Martin, Catherine R
APPLICANT: Plant Bloscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
                                                                                                                                                                                        APPLICANT: Edwards,
APPLICANT: Smith, A
APPLICANT: Bustos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
PRIOR APPLICATION NUMBER: GB 9716185.5 PRIOR FILING DATE: 1997-07-31 NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                     PRIOR FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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NAME: A. Anders Brookes
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                                                                                                                                                                                                                                                                                                                                                                    426 EKSRSGD 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 542 amino
TYPE: amino acid
STRANDEDNESS: sir
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COMPUTER: HP Vectra 486/33
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o. 6448043
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Bustos Guillen, Regla
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9410 Key West Avenue
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Query Match
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                              Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Sylvain Molneau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenbergh
TITLE OF INVENTION: Isolated DNA Encoding
TITLE OF INVENTION: Enzyme For Phage
TITLE OF INVENTION: Resistance
                                                                                                                                                                                 TELEFAX: (517) 347-410
TELEX: NO. 5824523e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Disketto
MEDIUM TYPE: storage
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                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,480
FILING DATE: December 30, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (517) 347-4100
                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                         MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 QKNRTGD 147
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/4 FILING DATE: April 19, 1995 CLASSIFICATION: 435
                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 20,931
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
 2 KSRTGD 7
                                                                                                                                                                  LENGTH:
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83.3%;
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71.4%;
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                                            Score 28; DB 2;
Pred. No. 1.2e+02;
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Pred. No. 1.1e+02;
2; Mismatches 0;
                               Mismatches
                                                          Length 288
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                               Gaps
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RESULT 5 US-08-820-980-11

Application US/08820980

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US-08-826-439-11

; Sequence 11, Application US/08826439

· batant No. 5972673
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: ACER
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette,
MEDIUM TYPE: storage
TITLE OF INVENTION: TITLE OF INVENTION:
                                      APPLICANT: Sylvain Moineau, Shirley A. APPLICANT: Walker, Ebenezer R. Vedamuthu, APPLICANT: and Peter A. Vandenbergh
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: Quest 4.1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
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                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,
FILING DATE: April 19, 1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ian C. McLeod
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 20,931
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                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                           Linear
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83.3%;
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              Enzyme For Phage
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Pred. No. 1.26
1; Mismatches
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1.2e+02;
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               EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER APPLICATION NUMBER: 60/052,732
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 553,
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/227,357
                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/051,926 EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: PCT/US98/13684 EARLIER FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fischer et al. TITLE OF INVENTION: 123 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (517) 347-410
TELEX: NO. 5972673e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PZ010P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: storage
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,
FILING DATE: APP11 19, 1995
CLASSIFICATION: 530
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NAME: Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 215
STREET: 215
STRY; Okemos
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TELEPHONE: (J...
190AX: (517)
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STRANDEDNESS: Sir
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1997-07-08
NUMBER: 60/051,931
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Pred. No. 1.2e+02;
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; SOFTWARE: PatentI
; SEQ ID NO 553
; LENGTH: 55
; TYPE: PRT
; ORGANISM: HOMO 9
US-09-227-357-553
                                              RESULT 8
US-09-227-357-552
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Sequence 552, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
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FILING DATE:
APPLICATION N
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FILING DATE: 1997-09-1
APPLICATION NUMBER: 60
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                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/058,660 FILING DATE: 1997-09-12
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APPLICATION
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                                                                                                                                              Similarity 83.:
5; Conservative
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                                                                                                                                                                                                                                                        DATE: 1997-09-12
ID NOS: 672
ntIn Ver. 2.0
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E: 1997-09-12
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: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                NUMBER: 60/055,954: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER: 60/055,984
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RE FILING DATE: 1997-07-08
RE APPLICATION NUMBER: 60/051,920
RE FILING DATE: 1997-07-08
RE APPLICATION NUMBER: 60/052,733
RE FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/055,954
APPLICATION NUMBER: 70/055,954
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APPLICATION NUMBER: 60/055,950
FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,947
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APPLICATION NUMBER: 60/055,953
TT TNG DATE: 1997-08-18
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APPLICATION NUMBER: 60/051,931
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,932
FILING DATE: 1997-07-08
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FILING DATE: 1999-01-08
APPLICATION NUMBER: PCT/US98/13684
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/051,926
FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/052,795
FILING DATE: 1997-07-08
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FILING DATE: 1997-09-12
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APPLICATION NUMBER: 60/055,723
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,930
FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/051,929
FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/1
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RESULT 10
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                                                                     Sequence 42, Application US/09361707 Patent No. 6258937 GENERAL INFORMATION:
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REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
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LENGTH: 174 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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165 ESRTGD 170
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STATE: Massa
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Wands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR NUMBER OF SEQUENCES: 117
                                                      APPLICANT: Tong, Shuping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
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Pred. No.
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Pred. No. 1.2e+02;
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APPLICANT:
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;; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 42: US-09-361-707-42
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                 Patent No. 5840577
NUMBER OF SEQUENCES:
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SEQUENCE CHARACTERISTICS:
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                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/462,481
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                               ADDRESSEE: Russell
STREET: 200 East Brown
CITY: Fort Lauderdale
STATE: Florida
                                      FILING DATE
                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                            COUNTRY: U
ZIP: 33301
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Local Similarity 83.3%;
es 5; Conserva+***
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REGISTRATION NUMBER: 34,31(
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
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APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08462481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 174 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                       200 East Broward Boulevard
                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hassel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silverman, Robert H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bret A.
                                                                                                                                                                                                                                                                                                                                                                                       Encoding
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Encoding Sequence Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 4;
Pred. No. 1.2e+02;
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                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198
FILING DATE: 18 FEB-1994
ATTORNEY/AGENT INFORMATION:
AMME: MANBO, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CLI1
TELECOMMUNICATION INFORMATION:
TELEPAX: 305/764/498
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 Entics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08436771 Patent No. 5861300
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,771
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 01 FILING DATE: 08-MAR-1993 ATTORNEY/AGENT INFORMATION:
 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
               TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 200 E. Broward
CITY: Fort Lauderdale
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 EKARTAD 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Manso, Peter REGISTRATION NUMBER:
                                                               LENGTH:
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200 E. Broward Boulevard
                                                              190 amino acids
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linear
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protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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08-MAR-1993
                             single
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71.4%;
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Pred. No. 1.3e-
1; Mismatches
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RESULT 14
US-08-487-797-7
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Best Local S
Matches 5
                                                                               Sequence 7, Application US/08487797 Patent No. 5866787
                                                                                                                                                                                                                                                Best Local Similarity 71.4 Matches 5; Conservative
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08434998 Patent No. 5866781
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
APPLICANT: SenGupta, Dibyendu N.
TITLE OF INVENTION: Transgenic Plants Co-Expressing A
TITLE OF INVENTION: Functional Human 2-5A System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
TITLE OF INVENTION: Cells and Methods
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 305/527/2498
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 200 E. Broward Boulevard CITY: Fort Lauderdale STATE: Florida
                                                                                                                                                                                   58 EKARTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Manso, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 EKARTAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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5; Conserv
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71.4%;
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Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
l; Mismatches 1
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                                                                                                                                                                                                                                                                                Length 190
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                                                                                                                                                                                                                                                Indels
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NUMBER OF SEQUENCES:

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US-08-701-005A-5
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                                                                                                                                                                                                                                Patent No. 58//ULA

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figg, Ernst & Kurz

STREET: 555 - 13th Street, N.W., Suite 701 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08701005A Patent No. 5877019
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Matches 5; Conserva
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Silverman, Robel
APPLICANT: Hassel, Bret A.
APPLICANT: Zhou, Aimin
APPLICANT: Zhou, Aimin
                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,005A
FILING DATE: 21-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: TITLE OF INVENTION: ent No. 5877019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: MANSO, PETER J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL
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ADDRESSEE: Holland & Knight
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 305/468-7811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/487,797
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
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CITY: Fort Lauderdale
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 EKARTAD 64
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ZIP: 33301
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71.4%;
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Encoding Sequence Therefor
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Pred. No. 1.3e+02;
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                                                      Query Match
Best Local Similarity
Matches 5; Conserv
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TELEPHONE: 202-783-6040
TELEPAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 08-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
58 EKARTAD 64
                                                                                                                                                                                                                                                                                                                                   NAME: Jondle, Robert REGISTRATION NUMBER:
                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                LENGTH:
                           1 EKSRTGD 7
                                                                                                                                                                                                                           190 amino acids
                                                       Conservative
                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                         single
                                                                   75.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                             US 08/028,086
                                                                                                                                                                                                                                                                                                                      N1255-111
                                                                  Score 27; DB 2; Length 190; Pred. No. 1.3e+02;
                                                    Mismatches
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Search completed: November 12, 2002, 17:01:41 Job time: 1.96137 secs

Gaps

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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Published_Applications_AA: *

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep: *

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *

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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

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13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *

14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *
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Gapop 10.0 ,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	· UT	4	ω	N	_	Result
26	26	27	27	27	27	27	27	27	27	27	27	27	28	28	28	31	31	36	Score
72.2	72.2	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	77.8	77.8	77.8	86.1	86.1	100.0	Query Match
68	83	2568	855	650	590	394	394	382	359	174	144	54	762	466	50	646	639	181	Query Match Length
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	DB
US-09-864-761-46399	US-09-864-761-42165	US-09-866-108-3	US-09-815-242-11930	US-09-943-671-29	US-09-943-671-25	US-09-946-034-2	US-09-863-475A-4	US-09-825-414-30	US-09-994-427A-11	US-09-818-066-42	US-09-815-242-11116	US-09-867-550-1596	US-09-925-299-998	US-09-741-669-303	US-09-864-761-37990	US-09-815-242-12304	US-09-815-242-5390	US-09-854-864-5	ID
Sequence 46399, A	Sequence 42165, A	Sequence 3, Appli	Sequence 11930, A	Sequence 29, Appl	Sequence 25, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 30, Appl	Sequence 11, Appl	Sequence 42, Appl	Sequence 11116, A	Sequence 1596, Ap	Sequence 998, App	Sequence 303, App	Sequence 37990, A	Sequence 12304, A	Sequence 5390, Ap	Sequence 5, Appli	Description

4 4 5	- 43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
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876	766	760	742	469	426	372	315	315	307	283	264	258	241	241	241	240	234	212	199	174	174	174	174	7 / 1
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US-09-815-242-11809 US-09-815-242-10269	-09-795	US-09-265-606-2	US-09-799-777-18	US-09-925-300-1494	US-09-864-761-42921	US-09-818-066-64	US-09-904-615-124	US-09-739-254-124	US-09-788-626-20	US-09-970-989-2	us-09-925-301-905	US-09-921-640-9	US-10-116-378-3	US-09-915-593-28	-915	US-09-915-593-6	-915	US-09-925-299-968	·921	818-066	US-09-818-066-47	818-066	US-09-818-066-45	US-U9-818-U55-49
Sequence 11809, A Sequence 10269, A		Sequence 2, Appli	18,	Sequence 1494, Ap	Sequence 42921, I	`	-		Sequence 20, Appl		90	9,	ω ·	28		Sequence 6, Appli	Sequence 2, Appli	Sequence 968, App	Sequence 6, Appli	•	•	Sequence 46, Appl	•	-

ALIGNMENTS

US-09-854-864-5

Sequence 5, Application US/09854864 Patent No. US20020081296A1

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RESULT 2
US-09-815-242-5390
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SEQ ID NO 5
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GENERAL INFORMATION:
APPLICANT: THEFILL, CANG
APPLICANT: THEFILL, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILLE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
                                                                                     Sequence 5390, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                   Matches
APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                102 EKSRTGD 108
                                                                                                                                                                                                                                                                                                                          100.0%; Score 36; DB 10; Length 181; Local Similarity 100.0%; Pred. No. 0.68; hes 7; Conservative 0: Mismatch-
                                                                                                                                                                                                                                                                       1 EKSRTGD 7
Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12304, Application US/09815242 Patent No. US20020061569A1
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TITLE OF INVENTION: Identification of Esse
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Versio
                                                                                                                                             PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                        TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                  PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                       PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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TYPE: PRT
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OR FILING DATE: 2000-03-21
OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR FILING DATE: 2000-10-23
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                           Carr, Grant J.
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Xu, H. Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                Daniel
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85.7%;
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Pred.
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28;
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; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 12304
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12304
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Best Local Similarity
Matches 6; Conserv
                              SOFTWARE: Annomax
SEQ ID NO 37990
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/864,761
                                                                              NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 EKSNTGD 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-08-03
                                                                                                                                                                    APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                    FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel, David K.
Chen, Wensheng
                                                                                                    DATE:
                                                                                DATE: 2001-01
ID NOS: 4911
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                                                                                                                                                                                                                          PCT/US01/00670
                                                                  Listing Engine
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Pred.
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FO

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APPLICANT: FOISYTH, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: CONSEN, Kari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITEA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEG ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Thes 5; Conserv
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                                                          ; TYPE: PRT; ORGANISM: Homo sapiens US-09-925-299-998
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US-09-925-299-998
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US-09-741-669-303
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US-09-741-669-303
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                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                           PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 998
LENGTH: 762
                                                                                                                                                                                                                                                                                                                                                                            Sequence 998, Application US/09925299 Patent No. US20020055627A1
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Query Match
Best Local Similarity
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nes 5; Conserv
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EXPRESSED IN FETAL LIVER, SIGNAL = 0.65
EXPRESSED IN LUNG, SIGNAL = 0.65
EST_HUMAN HIT: AU156079.1, EVALUE 2.20e+00
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71.4%;
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71.4%;
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    Mismatches

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Pred. No. 9.3;
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Pred. No.
   Score 28; DB 10;
Pred. No. 1.5e+02;
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-867-550-1596
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APPLICANT: Mehraban, Fuad,
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells of Invention: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USN 60/208,427
PRIOR APPLICATION NUMBER: USN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FASTSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                  PRIOR
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                  OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/257,931
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick, John D. Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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for Windows Version 4.0

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RESULT 10
US-09-994-427A-11
· Sequence 11, Application US/09994427A
                                                                                                                                                   Query Match
Best Local Similarity
"---hes 5; Conserv
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US-09-818-066-42
Sequence 42, Application US/09818066
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Best Local Similarity 83...
""" hes 5; Conservative
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SOFTWARE: FastSEQ for
SEQ ID NO 11116
LENGTH: 144
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INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UMBER: US/09/818,066

FILING DATE: 27-Mar-2001

FILING DATE: 27-Mar-2001
                                                                                                        165 ESRTGD 170
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                                                                                                                                     2 KSRTGD 7
                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Janis K.
RECISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION IMFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNETY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                          TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 542-8906
                                                                                                                                                                   Conservative
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Pred. No.
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Query Match
Best Local Similarity
""" 5; Conservi
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SEQ ID NO 11
LENGTH: 359
TYPE: PRT
ORGANISM: Mus musculus
US-09-994-427A-11
                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas syringae US-09-825-414-30
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                                                                                                                                                                      US-09-863-475A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/825,414
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/194,160
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 60/224,604
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/249,548
PRIOR FILING DATE: 2000-11-17
                                                                                 Sequence 4, Application US/09863475A
PATENT NO. US20020102688A1
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application U Patent No. US20020083489A1 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Geron Corporation
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 083,002
CURRENT APPLICATION NUMBER: US/09/994,427A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES FILE REFERENCE: 19603/3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COllmer, Alan
APPLICANT: Alfano, James R.
APPLICANT: Charkowski, Amy O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 382
                                                                                                                                                                                                                                                          197 EKGRAGD 203
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                  1 EKSRTGD 7
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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIOS, OR AS PREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09825414
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71.48;
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71.4%;
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Pred. No. 1.2e+02;
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Length 382;
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RESULT 13
US-09-946-034-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09946034 Patent No. US20020152488A1 GENERAL INFORMATION:
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Matches 5; Conservative
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Best Local
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/863,475A
FILING DATE: 24-May-2001
CLASSIFICATION : CUNKNOWN>
PRIOR APPLICATION NUMBER: 07/914,281
APPLICATION NUMBER: 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT IMPORMATION:
NAME: LAVAlleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
BEFERENCE COCKET NUMBER: 3263-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 EKGRNGD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
               ZIP: 30309-4530

COMPUTER READABLE FORM:
MEDIUM TYPE: FlOppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/946,034
FILING DATE: 04-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENETICALLY ENGINEERED ANIMALS FOR USE AS ORGAN DONORS
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cooper, David K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                       CITY: Atlanta
STATE: GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                   STREET: 1100 Peachtree Street, Suite 2800
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Patrea L. Pabst
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71.4%;
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Pred. No. 1.2e+02;
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                                                                                                                                        SEQ ID NO 25
LENGTH: 590
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-943-671-25
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                                                                      Matches
                                                                                                        Query Match
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/093,491
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: 60/110,941
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/943,671 CURRENT FILING DATE: 2001-08-31 PRIOR APPLICATION NUMBER: 09/232,191 PRIOR FILING DATE: 1999-10-14
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WHI97-21p3ME
                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stahl, Andreas
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450 KDRTGD 455
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                                                                     Local Similarity
nes 5; Conserv
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                                   2 KSRTGD 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Pabst, Patrea L. REGISTRATION NUMBER: 3
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                                                                      Conservative
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71.4%;
                                                                                     75.0%;
83.3%;
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Pred. No. 1.2e+02;
0; Mismatches 2
                                                                                   Score 27;
Pred. No.
                                                                     Pred. No. 1.80
); Mismatches
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US-09-943-671-29

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; Sequence 29, Application US/09943671 patent No. US/0020106733A1 ; GENERAL INFORMATION: APPLICANT: Stahl, Andreas

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APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WH197-21PAME
CURRENT APPLICATION UNMBER: 05/09/943,671
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 05/232,191
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 60/233,191
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: 60/233,191
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37
SOFTWARR: FastSEQ for Windows Version 3.0
SEQ ID NO 29
SEQ ID NO 29
SEQ ID NO 29
CHEGTH: 650
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-943-671-29
Ouery Match
Best Local Similarity 83.3%; Pred. No. 22+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 50;
PRIOR FILING DATE: 1998-12-04
Search completed: November 12, 2002, 17:09:12
Job time: 1.54077 secs
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Perfect score:
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2222222117
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A; Molecule type: DNA A; Residues: 1-184 <LAA> A; Status: preliminary

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ALIGNMENTS

N;Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C;Accession: \$43486; \$31208; \$36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1134, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is
A;Reference number: \$43486; MUID:94218235; PMID:8165126
A;Accession: \$43486

bid

B-cell maturation factor - human

S43486

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A;Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245 R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi EMBO J. 11, 3897-3904, 1992 A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(A;Reference number: S31208; MUID:93010984; PMID:1398583 A;Accession: S31208
RESULT 2
A69829
ABC transporter (ATP-binding protein) homolog yheI - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C;Date: 05-0ec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C;Accession: A69829
C;Accession: A69829
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A:Map position: 16p13.1-16p13.1
A:Introns: 44/1; 93/1
C:Superfamily: human B-cell maturation factor
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A; Residues: 4-184 <LA3>
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A; Residues: 1-184 <LA2>
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lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanion, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serojakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Zamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: cv. R; Shinozaki, K.; Ohme, M.; Deno, H.; Kamogashira, T.; EMBO J. 5, 2043-2049, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain 168
C;Genetics:
A;Gene: yheI
A;Gene: yheI
C;Superfamily: Escherichia coli ABC transporter mdlA;
C;Keywords: ATP; nucleotide binding; P-loop
F;354-548/Domain: ATP-binding cassette homology <ABC>
F;371-378/Region: nucleotide-binding motif A (P-loop)
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RESULT
S07137
                                                                                                                                                                                                                                                                           A:Start codon: TTC
C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2
C:Keywords: chloroplast
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C;Species: chloroplast Nicotiana tabacum (common tobacco)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_
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Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma,
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A; Residues: 1-862 <SUG>
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1; Mismatches
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K.; Kusuda, J.; Takaiwa, F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          August 1986
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                        A; Residues:
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C;Accession: H89843
R;Kurodd, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hudson, G.S.; Holton, T.A.; Whitfeld, P.R.; Bottomley, W. J. Mol. Biol. 200, 639-654, 1988
A;Title: Spinach chloroplast rpoBC genes encode three subunits A;Reference number: A29959; MUID:88316931; PMID:3045324
A;Accession: A29959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: cnroroptus;
C;Keywords: chloroplast;
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Blochem. J. 236, 453-460, 1986
A;Title: Pea chloroplast DNA encodes homologues of Escherichia A;Reference number: S07137; MUID:88323089; PMID:3530249
A;Accession: S07137
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                                                                                                                                                                                                                                                                                          hypothetical protein SA0674 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genome: chloroplast CNA-directed RNA polymerase beta'-2 C;Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 C;Keywords: chloroplast; nucleotidyltransferase; transcription
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A;Residues: 1-1163 <COZ>
A;Cross-references: EMBL:X03912; NID:g12137;
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A; Residues: 1-1361 <HUD>
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                              A; Molecule
                                                    A;Status: preliminary
                                                                             A; Accession:
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type: DNA 1-646 <KUR>
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GB:BA000018; PID:g13700610; PIDN:BAB41907.1;

GSPDB:GN00149

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; I ansen, N.F.; Hughes, B.; Hultar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosomer of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                           A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; PMID:11743193
A;Accession: AE3173
                                                                                                                                                                                                                                                                                                                                                 C;Accession: AE3173
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; I
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C; Superfamily:
                                                                                     A;Cross-references: GB:AE008687; PIDN:AAL45803.1; PID:g17743541; GSPDB:GN00188 A;Experimental source: strain C58 (Dupont)
                                                                                                                                A; Molecule type: DNA
A; Residues: 1-92 < KUR>
                                                                                                                                                                                                                                                                 A; Authors: Yoo, H.; Tao, ster, E.W.
                                                                                                                                                                                                                                                                                                          ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Agrobacterium tumefaciens
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A; Residues: 1-1195 <STO>
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probable kasein kinase (EC
N;Alternate names: protein
                                          T04265
                                                                   RESULT
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2.7.1.-) - Arabidopsis thaliana F20B18.210

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C;Accession: C97289
C;Accession: C97280
C;Accession: C97280
C;R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.; Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A:Deference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <KUR>
                                                                                                                                                                                                                                                                                                                          R;DelVecchio, V.G.; Kapatral, V.; Re.; Mazur, M.; Goltsman, E.; Selkov, Proc. Natl. Acad. Sci. U.S.A. 99, 44
A;Title: The genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                  glycosyl transferase (EC 2.4.1.-) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C:Cate: 01-Feb-2002 *sequence_revision 01-Feb-2002 *text_change 01-Feb-2002 C;Accession: AH3650
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A;Molecule type: DNA
A;Residues: 1-160 <KUR>
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C;Accession: C97289
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C97289
                                                                                                                                    A; Map position:
C; Keywords: glyo
                                                                                                                                                                                                                                                                                           A; Reference number: AD3252; A; Accession: AH3650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein CAC3165 [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum
                                                                                                                                                                       A; Gene: BMEII1129
                                                                                                                                                                                         C; Genetics:
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85.7%;
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, 443-448, 2002
the facultative
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lzer, P.H.; Hagius, S.; O'Callaghan, I
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D.; Le
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C;Species: Arabidop
C;Date: 30-Apr-1999
C;Accession: T04265
R;Bevan, M.; Rose,
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E72268
E72268
astByChuR-related protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Dete: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
C;Dete: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
C;Accession: E72268
C;Accession: E72268
C;Accession: E72268
C;Accession: E72268
A;Molecule type: DNA A;Molecule type: DNA A;Residues: I-526 <GEN> A;Residues: I-526 <GEN> A;Cross-references: EMBL:Z46660; NID:g575702; PID:g575717; MIPS:YML086c R;Huh, W.K.; Kim, S.T.; Kim, J.Y.; Hwang, S.W.; Kang, S.O. submitted to the EMBL Data Library, November 1995
                                                                                                   C;Accession: S49641; S61944
R;Gentles, S.; Bowman, S.
submitted to the EMBL Data I
A;Reference number: S49627
A;Accession: S49641
                                                                                                                                                                                                  L-galactonolactone oxidase (EC 1.1.3.24) - yeast (S
N;Alternate names: D-arabinono-1,4-lactone oxidase;
C;Specles: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995
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S49641
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A:Note: F20B18.210
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase
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A; Residues: 1-463 <ARN>
A; Cross-references: GB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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A; Residues: 1-450 <BEV>
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Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 14-Sep-2001
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6; Conser
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215263
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se: cultivar Columbia; BAC clone F20B18
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85.7%;
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Pred. No.
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Database, March 1999
                                                                                                                                           November 1994
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68;
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  A;Cross-references: GB:AE006469; PIDN:AAK65023.1; PID:g14523453; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Gallbert, F:, Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hupela, D:, Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
                                                                                                                                                                                                                                                                                                                                                                              RESULT
E95307
                                                                                                                                                                             A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Accession: E95307
                                                                                                                                                                                                                                      R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
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C; Superfamily:
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A; Residues: 1-526 <HUH>
                                                                                                                     A; Molecule type: DNA
A; Residues: 1-316 < KUR>
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A; Cross-references: GB:
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                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                     hypothetical protein SMa0689 [imported] - C;Species: Sinorhizobium meliloti
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 13-Aug-1999
C;Accession: H70441
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: The complete genome of the hyperthermophilic bacterium A; Reference number: A70300; MUID:98196666; PMID:9537320 A; Accession: H70441 A; Status: preliminary; nucleic acid sequence not shown; translate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map positLon: 13L
C; Keywords: ascorbic acid biosynthesis; oxidoreductase;
F;172-188/Domain: transmembrane #status predicted <TMM>
                                                                    24-Aug-2001 #text_change
                                                                                                                 Sinorhizobium meliloti (strain 1021) magapl
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C.; Abola, A.P.; Barloy-Hubler, C.; Surzycki, R.; Wells, D.H.;
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F.; Barloy-Hubl N.A.; Fisher, R.

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A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation
C;Genetics: A36089
A;Gene: SMa0689
A;Gene: SMa0689
A;Gene: Plasmid

Query Match
Best Local Similarity 71.4%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 221 EKARTGE 227

Search completed: November 12, 2002, 17:01:02

Job time: 2.08155 secs
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RPOD_STION
RPOD_ARATH
RPOD_SINAL
RPOD_TOBAC
ALO_YEAST
RPOD_GUITH
RLIS_ACST
GROW, YEAST
GROW, YEAST
GLUL_METTH
YCW1_YEAST
YS98_MYCTU
T2D2_STRPN
PI22_STRPN
PI22_STRPN
PI22_STRPN
PI23_STRGR
ALGL_PSESY
YDEU_CCOLI
MANC_ECOST
SP15_STRGR
MDLA_BUCAI
AFAM_MOUSE
Z143_HUMAN
COPA_ENTHR
UVRC_STRCO
ITA1_HUMAN
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	1 Y5G7_CLOAB P2367 1 UX5G7_CLOAB P2367 1 UX5Z_YEAST P3277 1 CP2Z_COLGL 00037 1 YIHL_ECOLI P3213 1 YBBE_BACSU P5073 1 SUHB_SYNY3 P7415 1 ALGL_AZOVI P5213 1 ALGL_AZOVI P2333 1 SUFFI_MESVI 05219 1 GATR_MOUSE 09mum 1 SECY_AQUAE 06649 1 SECY_BUCAI P5757 1 LAMB_ECO57 08x5w
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Y5G7_CLOAB UGX2_YEAST CP22_COLGL YIHL_ECOLI YPBE_BACSU SUHB_SYNY3 ALGL_AZOVI GATR_MOUSE YCF1_MESVI SECY_BUGAE SECY_BUGAE SECY_BUGAE SECY_BUGAE SECY_BUGAE	P2367 P3277 00037 P5073 P7415 P7415 05219 P2333 09mum 06449 P5757 Q8x5w
	P23672 P32772 Q003711 P32133 P50731 P74158 Q52195 P23336 Q9mum0 Q9mum0 Q8x5w7

ALIGNMENTS

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y-terminal kinase, and p38	Inoue J., Devergne O., Tsapis A.; "TNF receptor family member BCMA (B cell maturation) associates with	Hatzoglou A., Roussel J., Bourgeade MF., Rogier E., Madry C.,	FUNCTION. MEDLINE=20363816: PubMed=10903733:	Genes Immun. 2:2/6-2/9(2001). [5]		thematosus and rheumatoid	, Hashimoto H., Tokunag		[4] SEQUENCE FROM N.A., AND VARIANT THR-153.	Genomics 60:295-308(1999).	in 12	Adams M.D.;	Desiattes Mays A., Cao Y., Xu R.X., Kang HL., Mitchell S.,	alush F., Brandon		SEQUENCE FROM N. A.	Nucleic Acids Res. 22:1147-1154(1994).	bidirectionally transcribed.";	"The BCMA gene, preferentially expressed during B lymphoid		SEQUENCE FROM N.A.	EMBO J. 11:3897-3904(1992).	;16)(q26;p13) translocation in a malignant T cell lymphom	"A new gene. BCM, on chromosome 16 is fused to the interleukin 2 gene	Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,	d#1396583;	TISSUE-Deriphoral blood lenkogytee and I wonb pode:			hordata; Craniata; Vertebrata;		maturation protein). TNFRSF17 OR BCMA OR BCM.	Η,	15-JUN-2002 (Rel. 41, Last sequence update)	(Rel. 26, Created)		_

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DISULFID
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20259066; PubMed-10801128; Gross J.A., Johnston J., Mudri S., Madden K., Xu W., Parrish-Novak J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "B cell maturation protein is a receptor for the tumor necrosis family member TALL-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
-i- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
Promotes B-cell surviyal and plays a role in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boyle W.J., Sarosi I., Hsu H., S
"APRIL and TALL-I and receptors
humoral immunity.";
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McCabe S., Qiu W.R., Kornuc M., Sanaldi G., Theill L.
Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.
"APRIL and TALL-I and receptors BCMA and TACI: syste
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shu H.+B., Johnson H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20381353;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 404:995-999(2000).
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                                                                                                                                                                                                                                                                                                                                                                          MAIN
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                                                                                                                                                                                                                                                                                                                                                                                                   lransmembrane;
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DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION TWHICH INVOLVES BCMA AND IL2.

SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type III membrane protein. and perinuclear Golgi-like structures.
TISSUE SPECIFICITY: Expressed in mature B-cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  humoral immunity. Activates NF-kappa-B and JNK. SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $31208; $31208.
$31209; $31209.
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184
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153
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INTERLEUKIN 2/BC
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
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CYTOPLASMIC (POTENTIAL)
TNFR-CYS.
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277AF11E2767D932
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01-OCT-1989
01-JUL-1993
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-I- FUNCTION: DNA-DEPENDENT RNA POLYMFRA
                                                                                                                                                                                                                                                                                                               the European Bloinformatics Institute. There are no use by non-profit institutions as long as its conmodified and this statement is not removed. Usage by
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OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
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                                                                                                               EKSRSGD
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7; Conser
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(Rel. 26, Last annotation update)
d RNA polymerase beta" chain (EC 2
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1; Mismatches
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P56764;
30-MAY-2000
30-MAY-2000
16-OCT-2001
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HSSP; Q9KWU6; 1HQM.
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
Pfam; PF01854; RNA_pol_A2; 2.
Transcription; DNA-directed RNA polymerase;
154768 MW; 19FF8C42BB1B17E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-88316931; PubMed-3045324;

Mediton G.S., Holton T.A., Whitfeld P.R.,

"Spinach chloroplast ropec genes encode
"Spinach chloroplast ropec.";
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PIR; AZ9959; AZ9959.
HSSP; Q9KWU6; 1HQM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chloroplast RNA polymerase.*;
J. Mol. Biol. 200:639-654(1988).
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NCBI_TaxID=3562;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmitz-Linneweber C., Maier R.M.,
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                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                          Eukaryota; Viridiplantae;
                                                                                              Chloroplast
                                                                                                                          Arabidopsis thaliana
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                            Brassicales;
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39, Last sequence update)
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                              Brassicaceae;
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09THV5;

16-OCT-2001

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ISSP; Q9KWUG; 1HQM.
ISSP; Q9KWUG; 1HQM.
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
Pfam; PF01854; RNA_pol_A2; 2.
Transcription; DNA-directed RNA polymerase; Chloroplast.
156365 MW; 7CBB5820163E2B9D CRC64;
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SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-20039611; PubMed-10574454;
Sato S., Nakamura Y., Kaneko T., Asamizu E.,
                                                                                                                                                 alba L.). Integration of a prokaryotic with organelle-specific functions."; Eur. J. Biochem. 267:253-261(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots: Rosid eurosids II; Brassicales: Rrassicales:
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                                                                                                                                                                                                                                                                                                     STRAIN=cv. Albatros; TISSUE=Cotyledon; MEDLINE=20069369; PubMed=10601874;
                                                                                                                                                                                                                                                                                                                                                                                                     eurosids II; Brassicales;
NCBI_TaxID=3728;
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                                                                                                                                                                                                       "The multisubunit chloroplast RNA polymerase A from mustard (Sinapis alba L.). Integration of a prokaryotic core into a larger complex
                                                                                                                                                                                                                                                                              Pfannschmidt T.,
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF
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                                              SUBSTRATES.
CATALYTIC ACTIVITY: N nucleoside triphosphate
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SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS
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OF DNA INTO RNA USING THE FOUR
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                                                                                                     FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCF OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
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     SUBUNIT:
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d RNA polymerase beta" chain (EC 2
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     IN CHLOROPLAST
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     POLYMERASE
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                                                                                                                                                                                                                                                                                                     STRAIN-cv. Bright Yellow 4;
Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Haya:
Shinozaki K., Ohme M., Chunwongse J., Obokata J
Matsubayashi T., Zaita N., Chunwongse J., Obokata J
Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng
Deno H., Kamogashira T., Yamada K., Kusuda J., Taka
Tohdoh N., Shimada H., Sugiura M.;
"The complete nucleotide sequence of the tobacco ch
its gene organization and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994
01-0CT-1994
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _TOBAC
                                                                                                                                                       MEDLINE-94003079; PubMed-8400137;
Olmstead R.G., Sweere J.A., Wolfe K.H.;
"Ninety extra nucleotide in ndhr gene of tobacco chloroplast DN;
summary of revisions to the 1986 genome sequence.";
Plant Mol. Biol. 22:1191-1193(1993).
-1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCI
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-cv. Bright Yellow 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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InterPro; IPR000722;
InterPro; IPR002879;
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prPro; IPR002879; RNA_pol_A?.
n; PF00623; RNA_pol_A?; 1.
pF01854; RNA_pol_A2; 1.
usferase; Transcription; DNA-d
JENCE 1384 AA; 157740 MW;
                                                                             SUBUNITS: ALPHA,
                                                                                                                                            SUBSTRATES
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6; Conserv
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(Rel. 30, Last sequence up
(Rel. 40, Last annotation
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85.7%;
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                                                                                            THE RNA
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MW; 9A7B4D02053E
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9A7B4D02053F4A80 CRC64;
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                                                                                              POLYMERASE IS
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kata J.,
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
Transferase; Transcription; DNA-directed RNA polymerase; Chloroplast.
SEQUENCE 1388 AA; 156840 MW; 41FD7F238913188C CRC64;
                                 This SWISS-PROT entry is copyright. It is proceed to the Swiss Institute of Bioinformatics the Swiss Institute. There is
                                                                                                                                                                                                                                                                                                                                                                                       "D-Erythroascorbic acid is an important Saccharomyces cerevisiae."; Mol. Microbiol. 30:895-903(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE O STRAIN-ATCC 24858 / WHIO1; MEDLINE-99140446; PubMed=10094636; Huh W.-K., Lee B.-H., Kim S.-T., K Hwang C.-S., Lee J.-S., Kang S.-O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; SaccSaccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  Gentles S., Bowman S., Barrell B.G., Rajandream M.A.; Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 200044; CAA77410.1; ALT_SEQ. HSSP; Q9KWU6; 1HQM. InterPro; IPR000722; RNA_pol_A. InterPro; IPR002879; RNA_pol_A2.
                                                                                                                                                                                           1,4-LACTONE AND L-GALACTONO-1,4-LACTONE.
-!- CATALYTIC ACTIVITY: D-arabinono-1,4-lactone
                                                                                                                                                                                                                     -!- FUNCTION: CAN OXIDIZE L-GULONO-1,4-LACTONE AS WELL
                                                                                                                                                                                                                                                              STRAIN-S288c
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-S288c / AB972;
                                                                                                                                                                                                                                                                                                       Submitted (DEC-1997) to
                                                                                                                                                                                                                                                                                                                      gamma-lactone oxidase."
                                                                                                                                                                                                                                                                                                                                "Identification of the yeast
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
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                                                                                          PTM: The N-terminus is blocked. SIMILARITY: Belongs to the oxygoxidoreductase family.
                                                                                                                                    PATHWAY: D-erythroascorbic acid bios SUBCELLULAR LOCATION: Mitochondrial.
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Kang S.-O.;
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/east genomic sequence encoding L-galactono-
                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases
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Pred. No.
                                                                                                                                                 acid
                                                                                                         oxygen-dependent FAD-linked
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39;
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                                                             Query Match
                                                                    2MBL; Arvascope 14CM.
HSSP; Q9KW16; 1HQM.
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01654; RNA_pol_A2; 2.
Pfam; PF01854; RNA_pol_A2; 2.
Pfam; PF01854; Transcription; DNA-directed RNA polymerase;
Pfam; PF01854; RNA_pol_A2; 2.
Pfam; Pf01855; RNA_pol_A2; 2.
Pfam; Pf01854; RNA_pol_A2; 2.
Pfam; Pf01855; RNA_pol_A2; 2.
Pf01855; RNA_pol_A2; 
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15-DEC-1998
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ancestry with red algae.";

J. Mol. Evol. 48:236-244(1999).

-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPRO01575; Oxid FAD bind.
Pfam; PF01565; FAD binding_4; 1.
PROSITE; PS00862; Ox2_COVAL_FAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The plastid genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved synteny groups confirm its com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-99128221; PubMed-9929392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Cryptophyta; Cryptomonadaceae;
NCBI_TaxID=55529;
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-!- CATALYTIC ACTIVITY: N nucleoside
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                              Local
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SUBUNIT: IN CHLOROPLAST THE RN
SUBUNITS: ALPHA, BETA, BETA',
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S0004551; ALO1.
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417
526 AA;
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(Rel. 37, Last sequence update)
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d RNA polymerase beta" chain (EC
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FAD (COVALENT) (BY SIMILARITY).
A -> P (IN REF. 2).
; 942177A74A738EC8 CRC64;
Pred. No. le+
2; Mismatches
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Best Local
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Q9MUS7;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                  _MESVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001196; Ribosomal_L15.
Pfam; PF00256; L15; 1.
Pfam; PF01305; Ribosomal_L15; 1.
PIGRFAMs; TIGR01071; rp10_bact; 1.
PROSITE: PS00475; RIBOSOMAL_L15; FALSE_NEG.
Ribosomal protein; rRNA-binding; Complete proteome.
Ribosomal protein; rRNA-binding; Complete Proteome.
SEQUENCE 149 AA; 16572 MW; 12BBDA4E92D90357 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPLO OR AQ_1642
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Mesostigmatales;
NCBI_TaxID=41882;
[1]
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-!- FUNCTION: THIS PROTEIN
(BY SIMILARITY).
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30-MAY-2000
                                                                                              Mesostigma viride Chloroplast.
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16-OCT-2001
                                                                     Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
                                                                                                                                                RPOC2
                                                                                                                                                                    DNA-directed
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merase beta" chain (EC 2
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Mismatches
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Best Loc
Matches
STRAIN-S288c/ AB972;
STRAIN-S288c/ AB972;
Murakami Y., Naitou M., Hagiwara H., Shi
Sasanuma S.-I., Sasanuma M., Tsuchiya Y.
Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of
Saccharomyces cerevisiae.";
Nat. Genet. 10:261-268 (1995).
-I- FUNCTION: DNA-DEPENDENT RNA POLYMER,
OF DNA INTO RNA USING THE FOUR RIBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPOM_YEAST STANDARD; PRT; 1351 AA.
P13433;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase, mitochondrial precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Temleux C., Otis C., Turmer ...,

"Ancestral chloroplast genome in Mancestral chlor
                                                                                                                                                                                                                                                                                                                                                                            Masters B.S., Stohl L.L., Clayton D.A.; 
"Yeast mitochondrial RNA polymerase is 
bacteriophages T3 and T7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000722; RNA_POl_A.
InterPro; IPR002879; RNA_POl_A2;
Pfam; PF00623; RNA_POl_A; 1.
Pfam; PF01854; RNA_POl_A2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
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SEQUENCE 1
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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CATALYTIC ACTIVITY: N nucleoside triphosphate - N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNITS: ALPHA, BETA, BETA', AND BETA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQSKTGD 993
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5; Conserv
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71.4%;
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Pred.
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No. 1.
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/a Y., Soeda I
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1.6e+02;
                                                                                                                    chromosome
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Matches 6
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PIR; A27336; A27336.
HSSP; P00573; 1ARO.
SGD; S0001858; RP041.
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                       Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shmer G., Goyal A., Pietrrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                             15-JUL-1998
15-JUL-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (Sec or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               Methanobacterium thermoautotrophicum
Archaea; Euryarchaeota; Methanobacte;
Methanobacteriaceae; Methanothermoba
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                                                                                                                                                                                                                                                                                                                                              METTH
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PROSITE; PS00489; RNA_POL_PHAGE_2; 1.
Transferase; DNA-directed RNA polymerase;
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           J. Bacteriol. -!- FUNCTION:
                                                                                                                                                   STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                    NCBI_TaxID=187420;
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Pfam; PF00940; RNA_pol; 1.
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         MTH662
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- CATALYTIC A
[RNA](N).
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SIMILARITY: BELONGS TO
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6; Conservative
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(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
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Pred. No. 1.8e
0; Mismatches
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RESULT 13
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Best Local :
                                                                                                                      Matches
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01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Hypothetical 13.6 kDa protein in CPR4-SSK22 intergenic region
YCR071C OR YCR71C.
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P25642;
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Pfam; PF00543; P-II; 1.

PRINTS; PR00340; PIIGLNB.

PRODOm; PD001194; PII_glnB; 1.

PROSTITE; PS00638; PII_GLNB_CTER; 1.

Transcription regulation; Nitrogen fixation; Complete proteome.

SEQUENCE 115 AA; 12904 MW; 4E77B0AEA979BA53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1992) to the EMBL/GenBank/DDBJ-1- SIMILARITY: SOME, TO S.POMBE SPAC3H8.03.
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                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 121 AA; 13682 MW; F8E3304D6F38475A CRC64;
                                                                                                                                                                                                                                                                                               SGD; S0000667; IMG2
                                                                                                                                                                                                                                                                                                                           EMBL; X59720; CAA42269.1;
PIR; S19486; S19486.
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   69
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01-OCT-1996
01-OCT-1996
15-JUN-2002
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T2D2_STRPN
P09357;
01-MAR-1989
01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02021; UPF0102.

Pfam; PF02021; UPF0102; 1.

TIGREPAMs; TIGR00252; TIGR00252; 1.

Hypothetical protein; Complete prosequence 128 AA; 14222 km².
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE UPF0102 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaevat M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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01-OCT-1996 (Rel. 34, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein Rv2898c.
RV2898C OR MT2966 OR MTCY274.29C.
                                                                                                                      STRPN
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InterPro; IPR003509; U
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BBEB1657FB0AF571 CRC64;
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Matches 5
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MEDLINE-87002480; PubMed-3019562;

Lacks S.A., Mannarelli B.M., Springhorn S.S., Greenberg B.;

Lacks S.A., Mannarelli B.M., Springhorn S.S., Greenberg B.;

"Genetic basis of the complementary DpnI and DpnII restriction systems of S. pneumoniae: an intercellular cassette mechanism.";

Cell 46:993-1000(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Type II red
(R.DpnII).
DPNB.
                                                                                                                                                               EMBL; M14339; AAA88582.1; -.
PIR; B24372; B24372; B24372; B24372; B24372; B777; DpnIT; B7458E; Restriction system.
Hydrolase; Endonuclease; Nuclease; Restriction system.
SEQUENCE 288 AA; 33585 MW; F7346EEA6940EB33 CRC64;
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus.
NCBI_TaxID=1313;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Type II_restriction enzyme DpnII (EC 3.1.21.4) (Endonuclease DpnII)
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5; Conserv
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Pred. No. 54;
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Q8RWD7
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Q82969 bacillus sp
Q89744 staphylococ
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Q9c730 arabidopsis
Q9c649 arabidopsis
Q9c740 arabidopsis
Q8ctw7 pyrobacteri
Q8uki9 agrobacteri
Q97ee8 clostridium
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Q8x140 clostridium
Q9vd20 drosophila
Q8t8s8 drosophila
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ALIGNMENTS

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RESULT 1
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ID 0075
AC 0075
AC 0075
DT 01-J
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RN 
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Dorriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S.C., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Ra Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Fritz C., Fujita M., Fujita Y., Funas S., Galizzi A., Galieron N.,
RA Fritz C., Fujita M., Fujita Y., Funas S., Galizzi A., Galieron N.,
RA Glims Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hagan K., Haiech J., Itaya M., Jones L.,
AJOris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                007550 PRELIMINARY;
007550;
01-JUL-1997 (TrEMBLrel. 04, C
01-JUL-1997 (TrEMBLrel. 04, C
01-JUN-2002 (TrEMBLrel. 21, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-168;
Noback M.A., Terpstra P., Ho
Submitted (JUN-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holsappel S., Venema G., Bron
ne EMBL/GenBank/DDBJ databases
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RESULT 2
QBXL40
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Best Local S
Matches 6
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EMBL; Z99109; CAB12810.1; -.
HSSP; P13569; INBD,
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001140; ABC_tranprtrTM.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00664; ABC_tran; 1.
Pfam; PF00005; ABC_tran; 1.
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InterPro; IPRO
InterPro; IPRO
Pfam; PF00689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F., Ogasawara N.,
Submitted (NOV-1997) to
-I- SIMILARITY: BELONGS
(ABC TRANSPORTERS).
                                                                                                                                                                                                                             PubMed=11792842;
PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
Shiba T., Ogasawara sequence of Clostridium perfringens, an a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable calcium-transporting ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000006; ABC_transportr;
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168
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                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                          flesh-eater."
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ATP-binding; Hypothetical protein; Transport; Complete proteome
SEQUENCE 585 AA; 65111 MW; AB82FA64338F8161 CRC64;
                                                                                                                                          InterPro;
                                                                                  InterPro;
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                       c. Nati Acad. Sci. U.S.A. 99:996-10(
L; AP003189; BAB80908.1; --
arPro; IPR001757; ArPase_E1-E2.
erPro; IPR004014; Cation_ATPase.
erPro; IPR000661; H/K_Na/K_ATPase.
prPro; IPR001454; Hlgnase/hydrlase.
erPro; IPR001245; Tyr_pkinase
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  )1245; Tyr_pkinase.
Cation_ATPase_C; 1
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85.7%;
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the EMBL/GenBank/DDBJ databases.
TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33;
Pred. No.
                                                                                                                                                                                                  99:996-1001(2002)
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                                                                                                                                                                                                                                                        perfringens, an anaerobic
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RESULT
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McNort S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Sradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinsdeck G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng S.M., Weyers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Barandon R.C., Rogers Y.-H.C., Blazelj R.G., Champe M., Pfeiffer B.D., RA Abril J.F., Apgayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Bernan K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler A., Chandra I., Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Andrews B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dapan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Daylan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., Guan P., Harris N., Harri
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01-WAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
CG18427 protein.
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PROSITE;
PROSITE;
Complete
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Amanatides P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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CG18427 OR CG12757.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20196006; PubMed-10731132;
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6; Conser
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PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celniker S.E., Holt R.A., E
P.G., Scherer S.E., Li P.W.,
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Pred. No.
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kins R.A., Galle
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"atches 6; Conservations
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01-JUN-2002
01-JUN-2002
                                                                                                                                                                        Q9BBS7 PRELIMINARY; PRT; 1332 Am. Q9BBS7; O1-JUN-2001 (TrEMBLrel. 17, Created) O1-JUN-2001 (TrEMBLrel. 17, Last sequence update) O1-JUN-2002 (TrEMBLrel. 21, Last annotation update) RNA polymerase beta' subunit-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
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CG18427.
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               Lotus japonicus.
Chloroplast.
Ellaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Esermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
NCBI_TaxID-34305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Carcheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc. Ephydroidea; Drosophilidae; Drosophila.
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-I- CATALYTIC ACTIVITY: SN-GLYCEROL 3-PHOSPHATE + NAD(+) - GLYCERO PHOSPHATE + NADH.
-I- SIMILARITY: BELONGS TO THE NAD-DEPENDENT GLYCEROL-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY075291; AAL68158.1; -. SEQUENCE 1186 AA; 133529 MW; EC2606999C5EF36A CRC64;
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EMBL; AE003738; AAF55983.1;
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ENCE 1118 AA;
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6; Conservative
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85.7%;
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Last sequence update)
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Pred. No. 1.6e
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Pred. No. 1
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RESULT
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Best Local 9
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Best Local
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"Complete nucleotide sequence of the chromosome, representing plastome I of Eucenothera plastomes.";
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Pfam; PF01854; RNA_pol_A2; 2.
Chloroplast.
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MEDLINE-21082929; PubMed-11214967;
MEATO T., Kaneko T., Sato S., Nakamura Y
"Complete structure of the chloroplast
japonicus.";
DNA Res. 7:323-330(2000).
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01-OCT-2000
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STRAIN=ACCESSION MG-20;
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SEQUENCE
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01-JUN-2002
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InterPro; IPR0007879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
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MEDLINE=20309318; PubMed=10852478;
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InterPro; IPR002879;
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EMBL; AJ271079; CAB67153.1; -
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NCBI_TaxID=85636;
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                                                                                                                                                                   1386 AA;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation updatase beta', subunit.
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85.78;
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                                                                                                   88.9%;
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Pred.
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Pred. No. 1
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082969;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanalea: Solanalea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sun
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01-JUN-2002 (TrEMBLrel. 21, Last
01-JUN-2002 (TrEMBLrel. 21, Last
01-JUN-2002 (TrEMBLrel. 21, Last
RNA polymerase beta II subunit.
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Pfam; PFO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Wolbachieae; Wolbachia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolbachia sp. wRi.
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NCBI_TaxID=33113;
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Genomic organization o
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PF02033; RBFA; 1.
NCE 132 AA; 15102 MW; 24BCF
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Pred. No. 1.9e+02;
1; Mismatches 0;
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01-JUN-2001 (TIEMBLIFE! 1
01-MAR-2002 (TIEMBLIFE! 2
Hypothetical protein SAVO
SAVO719 OR SA0674
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01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
A2-5a orf1 (Fragment).
Bacillus sp.
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                                                                                                                  Q99VQ4
Q99VQ4;
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SOUTHWICK A., KARIII-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Sakurai T., Theologis A., Davis R.W.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY09316; AAM13159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 31.6 kDa protein.
ATIG58210
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of the cyclodextrin glucanotransferase gene from alkalophilic Bacillus sp. A2-5a and analysis of the raw starch-binding domain."; Appl. Microbiol. Blotechnol. 53:430-434(2000).
EMBL; AB015670; BAA31529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-20261044; PubMed-10803899;
Ohdan K., Kuriki T., Takata H., Okada S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
Bacillaceae; Bacillus.
NCBI_TaxID=1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8RWD7;
                                                                                                                                                                                                                                                            212
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                                                                                                                                                                                                                                                         EKSRVGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conserv
                                                                                                                                                                                                                                                                                                                                                                       Similarity
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B (TrEMBLrel.
l (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                       l protein.
281 AA; 31560 MW;
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                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27286 MW;
                          SAV0719
                                                                                                                                                                                                                                                                                                                                                                       86.1%;
85.7%;
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85.7%;
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                                             17, Created)
17, Last sequence up
20, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                         27EA3BE744F89528 CRC64;
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                                                                                                                                                                                                                                                                                                                                                    Mismatches
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annotation
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                                               update)
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RC STRAIN-CV. COLUMBIA;

RX MEDLINE-21016719; Pubmed-11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Chung M.E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.E., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Lee A., Lee J.M., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Askano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

San H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis

RT thaliana.",

RE EMBL; AC073943; AAG50957.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9C730;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
Hypothetical 135.5 kDa protein.
F16M22.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oyuchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus
Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lancet 357:1225-1240(2001).

EMBL: AP003360; BAB56881.1; -

EMBL: AP003131; BAB41907.1; -

InterPro; IPR000917; Sulfatase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9C730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mouse-ear cress).
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Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No.
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788FE36EB4528BB0 CRC64;
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RESULT
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ID Q8
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DT 01
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DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
Tsequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
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Best Local
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 141.0 kDa protein.
T18124.12.
Arabeta
Q8ZTW7;
Q8ZTW7;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001064; Crystallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 1195 AA; 135520 MW; 6EFE58DCE994D744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000).

EMBL, AC079131; AAG50760.1; -.

InterPro; IPRO01064; Crystallin.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 1246 AA; 140995 MW; BE23EE9DC47F3F88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. COLUMBIA;
MEDLINE=21016719; PubMed=11130712;
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                                                                                                           PRELIMINARY;
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85.7%;
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85.7%;
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21,
Created)
Last sequence up
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Pred. No.
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Pred. No. 2.9e+02
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Archaea; Crenarchaeota; Thermoprotei; Thermoproteales; Thermoproteaceae; Pyrobaculum.

51768 / DSM 7523;

Pyrobaculum aerophilum. Hypothetical protein PAE3058.

PAE3058.

NCBI_TaxID=13773; [1]

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RESULT 15
QBUKI
QBUKI
DT 01-JU
DT 01-JU
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DT 01-Bacte
OC Rhizo
OX AGEDLI
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Best Local S
Matches 6
                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
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MEDITINE-2160850; pubMed-11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almelda N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McCLelland E., Palmleri A.,

Kutyavin T., Levy R., Li M.-J., McCLelland E., Palmleri A.,

Raymond C., Rouse G., Saenphinmachak C., Wu Z., Romero P., Gordon D.

Raymond C., Rouse G., Saenphinmachak C., Wu Z., Romero P., Gordon D.

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

"Roster E.W.;
                                                                                                                                                                                                   Science 294:2317-2323(2001).
EMBL; AEO08936; AAL45803.1; -.
Plasmid; Complete proteome.
SEQUENCE 92 AA; 10349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid AT,
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens (strain C58 / ATCC 33970). Plasmid AT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8UKI9;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002792; TRAM.
Pfam; PF01938; TRAM; 1.
Hypothetical protein; Comp.
SEQUENCE 79 AA; 8695 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the hyperthermophilic crenarchaeon aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009908; AAL64642.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-IM2 / ATCC Pubmed-11792869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
21
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                                                                                                                                                                                                                                                                                                                               genome of the natural genetic engineer Agrobacterium tumefaciens
ERARTGD
                                              EKSRTGD 7
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6; Conserv
                                                                                                    Conservative
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27
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8695 MW; B36D5871B6C30143 CRC64;
                                                                                                                       83.3%;
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85.7%;
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                                                                                              Score 30; DB Pred. No. 25; 2; Mismatches
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Pred. No. 21;
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                                                                                                                                                                                                     51B37E9FD71DF6D2 CRC64;
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Search completed: November 12, 2002, 17:00:20 Job time : 4.13305~secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

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Minimum DB
Maximum DB
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                           score greater than
and is derived by analysis of the total score distribution
                                                    Pred. No.
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length: 2000000000
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239
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Listing first 45 summaries
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                                                                                                 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999_DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001_DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp~emb1/AA1985.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
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                      to have a being printed,
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Result No.	Score	Query Match I	Length DB	!	ID	Description.
1	239	100.0	51	23	AAE15485	Human B-cell matur
2	239	100.0	181	23	AAE15484	Human B-cell matur
ω	239	100.0	184	21	AAB08843	Amino acid sequenc
4	239	100.0	184	21	AAY94001	A human BCMA prote
51	239	100.0	184	22	AAE09241	Human BCMA protein
σ	239	100.0	184	22	AAE00506	Human B cell matur
7	239	100.0	184	22	AAB60698	Human BAFF recepto
8	239	100.0	184	22	AAY71979	
9	239	100.0	184	23	ABB81487	Human BCMA recepto
10	239	100.0	283	23	AAE15488	Human BCMA-immunog

	4 4	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
00.0	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	71.5	90.5	95.5	156	156	156	156	181	201	219	239	239
	28.2			•		•		•					•										29.9	•	•	•		•	•			91.6	0.	0.001
ų.	404	397	366	334	312	293	293	293	293	293	293	293	293	293	293	293	291	265	166	166	59	37	249	24	117	· 281	185	185	185	157	34	58	302	302
N.	2 3	23	23	23	23	23	23	23	23	23	23	22	22	21	21	19	23	22	23	19	23	23	21	23	23	23	23	22	21	22	23	23	22	22
AAEL5495	AA014136	AAE15498	AAO14132	AAO14133	AAO14135	AAU09900	AAE15493	AAU75408	AA014130	ABB81488	AAU99512	AAY71914	AAE09240	AAY94000	AAB36312	AAW75783	AAU10949	AAE09244	AAE15494	AAW75785	AAE15500	AAU10951	AAY94006	AAE15492	AAE15491	AAE15489	AAE15490	AAY71980	AAB08844	AAB60700	AAE15486	AAE15501	ААВ60699	AAE00507
Human TAC1 cystein		Human TACI-immunog			_	Human AGP-3 relate	Human transmembran	Tumour necrosis fa	Human transmembran	Human TACI recepto	Human TACI-IgG Fc	Human tumour necro	Human TACI protein	A transmembrane ac	Human neutrokine-a	Human lymphocyte s	AGP-3	Human TACI splice	Human TACI extrace	Human lymphocyte s	Human TACI cystein	Human AGP-3 recept	A murine ztnf4, a	Human-murine BCMA	Human-murine B cel	Mouse BCMA-human i	В	е в се		ř	cell	n B ce		Human BCMA-Immunoq

ALIGNMENTS

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RESULT 1
AAE15485
Human B-cell maturation (BCMA) protein extracellular domain.
                                                                            AAE15485;
                                                                                                                AAE15485 standard; peptide; 51
                                       12-MAR-2002
                                     (first entry)
                                                                                                                  A
A
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Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; human immunodeficiency virus; HIV; systemic lupus erythematosus; rheumatoid arthritis; atherosclerosis

Homo sapiens.

WO200187979-A2.

22-NOV-2001.

12-MAY-2000; 2000US-204039P 27-JUN-2000; 2000US-214591P 14-MAY-2001; 2001US-0214591 14-MAY-2001; 2001WO-US15567

(AMGE-) AMGEN INC

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RESULT 2
AAE15484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC protein (BCMA) activity in a mammai. The method comprises administering CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF CC family ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region CC of TACI or BCMA. The method is useful for inhibiting activity of TACI/CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell CC lymphoproliferative disorders, one or more solid tumours such as lung, CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI/CC antagonists are useful for treating lifenmention and immune function CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung CC (Crohn's disease, colitis), scleroderma, autoimmune disease (miltiple CC (Crohn's disease, colitis), scleroderma, autoimmune disease (miltiple CC sclerosis, rheumatoid arthritis, systemic lupus erythematocus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer CC with leucocyte infiltration of the skin or organs. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                           Human, transmembrane activator and intracellular CAML interactor, TACI, cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; panoreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention activator and
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                 WO200187979-A2.
                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                             Human B-cell maturation (BCMA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE15484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE15484 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                              Region
                                                                                                                                                                                                                                             rheumatoid arthritis; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCMA protein extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 10A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relates to a method for inhibiting TACI (transmembrane intracellular CAML interactor) and/or B cell maturatio
                                                                  /note= "Cysteine-rich consensus region; This is region is specifically claimed as SEQ ID NO: 7 in claim 1 of the specification" 52..72
                                                                                                                                                Location/Qualifiers 5..38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                      Transmembrane_domain
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Pred. No. 4.4e-22;
; Mismatches 0;
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AAB08843
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                                                                                                                                                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for inhibiting TACI (transmembrane cactivator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering can specific binding partner for APRIL (G70, a tumour necrosis factor TNF (Family ligand), having the consensus region of TACI BCMA, or the TACI/CE BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI cand/or BCMA in a mammal which is useful for treating B-cell or T-cell cand/or BCMA in a mammal which is useful for treating B-cell or T-cell cand/or BCMA in a mammal which is useful for treating B-cell or T-cell cand/or BCMA in a mammal which is useful for treating inflammation and immune function can act of the strong allergies, preumonia, atopic calseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic calseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic calsease, colitis, seleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, cancer with legecter is infiltration of the stin or crans the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAY-2000;
27-JUN-2000;
14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
                                                                                                                                  BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 10A; 94pp;
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WO200050633-A1
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                                                                                                                                                                                                                                                                          AAB08843;
                                                                                                                                                                                                                                                                                                            AAB08843 standard;
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                                                 Domain
                                                               Key
                                                                                                    Homo
                                                                                                                                                                                                       Amino acid sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ls numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with leucocyte infiltration of the skin or organs. The present
                                                                                                                                                                                                                                                                                                                                                                                                             1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
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                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCMA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AA;
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; 2000US-214591P.
; 2001US-0214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                         (first entry)
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                                               Location/Qualifiers 57..77
                                 'note= "putative transmembrane domain"
                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 239; DB 23;
Pred. No. 1.6e-21;
; Mismatches 0;
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RESULT 4
AAY94001
ID AAY9
XX AAY9
AC AAY1
XX 20-
XX A h
XX Hum
KW TIF
KW STI
KW ST
KW ST
KW SN
K
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Best Local
                                                                                                                                                                                                                                                                        Human; BR43x2; TACI receptor: extracellular domain; BCMA; B cell protein; transmembrane activator and CAMI-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF) *NB retor. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method is the promoter of the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A human BCMA protein, a B cell protein related to TACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY94001 standard; Protein;
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                                                                                                                                                                        immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identifying compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                               artery stenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEN HOSPITAL CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that modulate NF-kB expression and thus for drug
                                                                                                                             cces mellitus; Crohn's disease; hypertension; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 239; DB 21;
Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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WO200040716-A2

WO200160397-A1 Homo sapiens

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CC protein) receptor contains cysteine rich domain, and are used for chimbiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used combibiting stnf4 activity. Ztnf4 is a TNF ligand. They may also be used combibiting BR43x2, TACI or BCMA receptor-ligand engagement associated combibiting BR43x2, TACI or BCMA receptor-ligand engagement associated combibiting production. The antibody production is associated with an combibition of the state of the st
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAE09241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor TACI is a tumour necrosis factor (TNF) receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JAN-1999;
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                                                                                                                                                                              Human; TNF;
TNFR; TACI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises
                                                                                                                                                             autoimmune disease; rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                     Human BCMA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (2YMO ) ZYMOGENETICS
                                                                                                                                    psoriasis.
                                                                                                                                                                                                                                                                                                    19-NOV-2001
                                                                                                                                                                                                                                                                                                                                                     AAE09241;
                                                                                                                                                                                                                                                                                                                                                                                                 AAE09241 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-452538/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                 tumour necrosis factor; TALL-1; APRIL; TNF BCMA; therapy; cancer; leukaemia; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 152; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 1.7e-21;
Mismatches 0;
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                                                                                                                                                                                                       TNF receptor;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                  Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TWF (tumour necrosis factor) especially TALL-1, APRLI and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, as the supplementation of the second of themselves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exposing the cells
  06-OCT-1999;
11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human B cell maturation protein (BCMA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE00506 standard; Protein;
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22-AUG-2000;
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                                                                         05-OCT-2000; 2000WO-US27579
                                                                                                                             12-APR-2001
                                                                                                                                                                             WO200124811-A1
                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE00506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psoriasis and lupus erythematosus. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting
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DB; AAD15902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
42; Conserv
                                                                                                                                                                                                                                                                                   necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or neutralizing TALL-1 or APRIL polypeptide biological for treating autoimmune disorders and cancer, comprises the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig
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99US-0157933
2000US-0181807
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2000US-0226986
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                                                                                                                                                                                                                                                                                factor;
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                                                                                                                                                                                                                                                                                   BCMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .09;
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                                                                                                                                                                                                                                                                                   cell maturation
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. No. 1.7e-21;
smatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ancer, comprises agonists or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as CC A Proliferation protein (BCM or BCMA) antagonist that antagonises the cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is CC useful for treating undesired cell proliferation such as cancer or CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, colon carcinoma e.g. cardiovascular CC prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular CC disease, renal disorders, B-cell lympho-proliferative disorders, cardiovascular CC disease, renal disorders, organ transplantation, inflammation and CC human immunor ersponse involving a signalling pathway between CC altering an immune response involving a signalling pathway between CC altering an immune response involving a signalling pathway between the present sequence is human APRIL-R also useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                              Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lumby and concert force the service of the service of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering composition comprising A Proliferation Inducing Ligand Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human BAFF receptor (BAFF-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB60698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB60698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of treating a mammal for a condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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(APRIL-R) antagonist -
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(APOT-) APOTECH R & D SA.
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                                                                                                                                        Homo sapiens
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Pred. No. 1.7
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. NO. 1.7e-21;
smatches 0;
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11-FEB-2000;
18-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Fig 1; 59pp; English.
                                                    Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; Therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin_dependent_diabetes_mellitus;
                                                                                                                                                  Human B cell maturation factor (BCMA) protein.
                                                                                                                                                                                                                                                                    AAY71979 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOJ ) BIOGEN INC. (APOT-) APOTECH R &
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                   thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
                                                                                                                                                                                          28-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 42; Conserv
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2000US-0181684.
2000US-0183536.
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Pred. No. 1.7e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to Tumour necrosis factor (TNF) and Apol-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate monocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune thrombour treating in the content of t
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01-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not by brain, muscle, heart, lung, kip pancreas, testis and placenta. BCMA mRNA is absent in the pro-B lymphocyte stage but its expression increases with B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 37; Page 104-105; 112pp; English.
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The present sequence is a human B
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DB; AAD02125.
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Pred. No. 1.7
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02-SEP-2002

(first entry)

BCMA receptor

related protein

SEQ ij NO: 7

TACI;

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The present invention describes a human tumour necrosis factor receptor CC designated Ztnf2(I), (I) has cytostatic, immunosuppressive, antichiabetic, antirhelmamatory, neuroprotective, antidiabetic, CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (I) can be used for CC inhibiting, in a mammal, the activity of a ligand that binds Ztnf12 CC (e.g. ZTNF4), for treating disorders and diseases associated with B CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for CC inhibiting the proliferation of tumour cells. (I) is useful for treating CC autoimmune disorders such as systemic lupus erythematosus, myasthenia CC remail disease such as systemic lupus erythematosus, myasthenia CC remail disease such as glomerulonephritis, vasculitis, chronic lymphoid cc renal disease such as glomerulonephritis, vasculitis, chronic lymphoid CC leukacmia, nephritis, and pyelonephritis, and for treating renal CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or CC amyloidosis, hypertension, large vessel diseases, graft rejection and Crohn's diseases, (I) is useful for modulating the immune system, for regulating B cell responses and CC development, for modulating development of other cells, antibody CC production and cytokine production, and for modulating T and B cell Cc communication. The present sequence represents a protein which is given in the exemplification of the present invention.
                                                                                                                           Matches
                                                                                                                                                        Query Match
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20-DEC-2000;
28-JUN-2001;
29-AUG-2001;
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                             MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated human tumor necrosis factor receptor polypeptide, termed 12, useful for treating autoimmune disorders, emphysema, end renal failure or renal disease and lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ztnfr12;
                                                                                                                       1 Similarity
42; Conser
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2000US-257131P.
2001US-301715P.
2001US-315565P.
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                                                                                                                           Conservative
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Pred. No. 1.7
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                                                                                                                                                                                     CC protein (BCMA) activity in a mammal. The method comprises administering CC a specific binding partner for APRIL (670, a tumour necrosis factor-TNF (family ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region CC of TACI or BCMA. The method is useful for inhibiting activity of TACI CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell CC lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple colerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atheroscierosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein-immunoglobulin Fc region fusion protein.
                           Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 10B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               administering a binding family ligand .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-066686/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis; atherosclerosis; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E,
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1 Similarity 100 42; Conservative
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2001US-0214591.
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11-FEB-2000;
30-JUN-2000;
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Chimeric
The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulate by APRIL. It is also useful for treating autoimmune diseases (Grave's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; murine; tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
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                                                                                                                                                                                                                                                                                                                                                           Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering composition comprising A Proliferation Inducing Ligand Receptor
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24..30
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76..30
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                     immune-related disorder; B-cell growth inhibitor;
B-cell maturation inhibitor; immunoglobulin production inhibitor;
autoimmune disorder; B-cell lymphoproliferative disorder; hypertensic
renal disorder; immunosuppressive disorder; HIV infection;
organ transplantation; antiinflammatory; systemic lupus erythematosus
autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
                                                                                                                                                                                                                                                       17-AUG-1999;
11-FEB-2000;
18-FEB-2000;
                                                                                    Inhibiting dendritic cell-induced B-cell growth, lympho-proliferative disorder by administering Barbolypeptide, chimeric molecule comprising receptor.
                                                                                                                                                                                                                   (BIOJ )
                                                                                                                                                                                                                                                                                                                                                                                   Chimeric -
Chimeric -
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                                                                                                                                                                                          маскау ғ,
                                                                                                                                                                                                                                                                                                         16-AUG-2000; 2000WO-US22507
                                                                                                                                                                                                                                                                                                                                                           WO200112812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BAFF-R; BAFF receptor; TNF family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                         2001-202866/20.
DB; AAF59999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IgG signal/human BAFF-R/human IgG
                                                                                                                                                                                                                   APOTECH R & D
                                                                                                                                                                                                                               BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
                                                                                                                                                                              ŗ
                                                                                                                                                                                                                                                                                                                                                                                   Mus
                                                                                                                                                                                        Browning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                     ; 99US-0149378.
; 2000US-0181684.
; 2000US-0183536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                    SA.
                                                                                                                                                                                           Ambrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .08;
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Pred.
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                                                                                                                                                                                        Tschopp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein,
                                                                                                                                                                                        'n
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0;
                                                                                     h, maturation and B-cell
BAFF-receptor
ptor or anti-BAFF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                          Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human immunoglobulin cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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as BCMA) protein, or a treatment of a variety

homolog Fig

2;

59pp; English.

invention relates to the use of a BAFF receptor (BAFF-R, also known BCMA) protein, or a BAFF-R fusion protein as an agent for the atment of a variety of immune-related disorders. BAFF-R is a member

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                         12-MAY-2000;
27-JUN-2000;
14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and in the treatment of autoimmune disorders, B-cell jymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signaling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related disorders. BAFF-R, fusion proteins containing it, and specific antibodies can be used for inhibiting B-cell growth, cell-induced B-cell growth and maturation, and immunoglobulin
Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor % \left( 1\right) =1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              progressive glomerulonephritis, and lymphomas, Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents the BAFF-R fusion protein BAFF-R-FC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
                                                                                                                                        Theill LE,
                                                                                                                                                                                  (AMGE-)
                                                                                                                                                                                                                                                                                                                    14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                22-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                            WO200187979-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human B cell maturation protein cysteine rich extracellular region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE15501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE15501 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising a mouse IgG-kappa signal sequence, of human BAFF-R and a human IgG Fc sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 68
                                                                                            2002-066686/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane activator and intracellular CAML interactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Conser
                                                                                                                                                                                    AMGEN INC
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                                                                                                                                                                                                                            ; 2000US-204039P.
; 2000US-214591P.
; 2001US-0214591.
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                                                                                                                                                                                                                                                                                                                    2001WO-US15567.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 239; DB 22;
Pred. No. 2.8e-21;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dendritic
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Inhibiting activity of

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cell maturation protein

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                  12-MAY-2000;
27-JUN-2000;
14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                           Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE15486
                              WPI; 2002-066686/09
                                                               Theill LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; transmembrane activator and intracellular CAML interactor; TACI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                        14-MAY-2001; 2001WO-US15567.
                                                                                                                                                                                                                                                                           WO200187979-A2
                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                 lymphoproliferative disc
prostate; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE15486 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
                                                                                                                                                                                                                                                                                                                                                                                                   allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                            sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Similarity
38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                      B cell maturation protein; BCMA; tumour necrosis ractor; inr, ferative disorder; tumour; lnng; gastrointestinal; pancreatio; inflammation; immune disorder; diarrhoea; postriasis; collitis; nflammation; immune disorder:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 13; 94pp; English
                                                                 Yu G;
                                                                                                                                  2000US-204039P.
2000US-214591P.
2001US-0214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.6%;
                                                                                                                                                                                                                                                                                                                                                atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 219; DB 23
Pred. No. 1.4e-1
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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1.4e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Sequence

34 AA;

human

BCMA protein cysteine-rich consensus region.

CC protein (BCMA) activity in a mammal. The method comprises administering CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF CC family ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region CC of TACI or BCMA. The method is useful for inhibiting activity of TACI/CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell CC lymphoproliferative disorders, one or more solid tumours such as lung, CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI/CC antagonists are useful for treating inflammation and immune function CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung CC disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autolimune disease (Crohn's disease, colitis), scleroderma, autolimune disease (maltiple CC sclerosis, rheumatoid arthritis, systemic lupus erythematorsus), fungal, CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer CC with leucocyte infiltration of the skin or organs. The present sequence

The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation

Claim 1;

Fig 10A; 94pp; English.

activator and administering

intracellular cyclophilin ligand interactor, by a binding partner for APRIL, a tumor necrosis factor

family ligand

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RESULT 15
AAB60700
XX AAB60
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immuno-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB60700 standard; Protein; 157
MacKay F, Browning J,
                                                                                                                                                                          11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                               17-AUG-1999;
                                                                                                                                                                                                                                                                                                                     16-AUG-2000; 2000WO-US22507.
                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                     BIOGEN INC.
APOTECH R &
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2000US-0183536
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   Ambrose C,
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Pred. No. 1.3e-17;
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   Tschopp J,
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   Schneider
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39 42

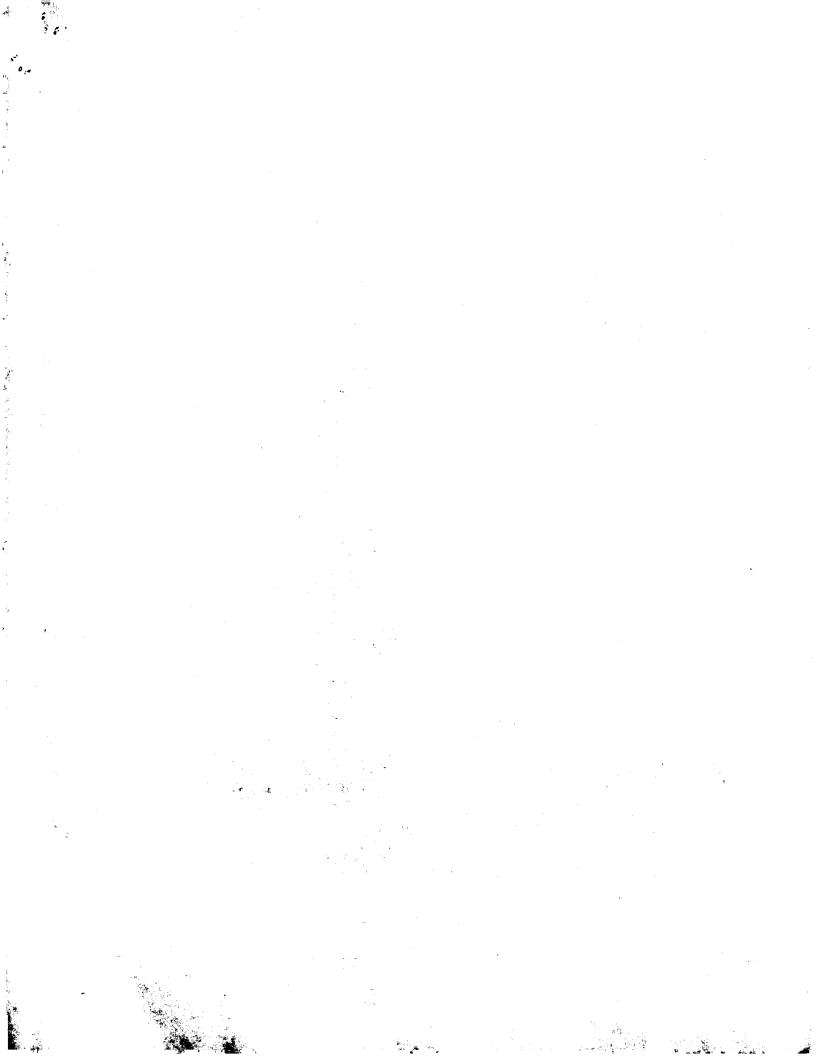
2

Search completed: November 12, Job time: 17,0429 secs

2002,

16:58:33

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as BCMA) protein, or a BAFF-R fusion protein as an agent for the Ct treatment of a variety of immune-related disorders. BAFF-R is a member of the TMF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-CC specific antibodies can be used for inhibiting B-cell growth, dendritic call-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. THe BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R proteins or BAFF-R and baff-I antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R conhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders. The
  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide, chimeric molecule comprising receptor antibody homolog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thompson
                                                                                        Sequence
                                                                                                                                  acids shorter than that given in AAB60698.
                                                                                                                                                       present sequence represents a human BAFF-R protein sequence as encoded
by plasmid PJST535. However, this BAFF-R protein sequence is 27 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 3; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor
                         Local
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Similarity
36; Conserv
                                                                                           157
  Conservative
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                       75.7%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the use of a BAFF receptor (BAFF-R, also known
  0
                     Score 181; DB 22; Pred. No. 1.7e-14;
  Mismatches
  0;
                                          Length 157;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or anti-BAFF-R
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Gaps
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Minimum
Maximum
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No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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       22543311443113155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     seq length: 0 seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Match
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     Issued_Patents_AA:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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   US-08-810-572A-6
US-09-290-333-6
US-09-290-333-2
US-08-810-572A-2
US-08-290-333-2
US-08-276-290-811-4
US-08-824-996-2
US-08-99-811-4
US-08-515-895-33
US-08-515-133A-33
US-09-042-105-18
US-08-795-430-8
US-08-795-430-8
US-08-716-310-33
US-08-716-301-4
US-08-465-380-4
US-08-465-380-4
US-08-486-397-40
US-08-486-397-40
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214.236 Million cell updates/sec
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Query Match
Best Local Similarity
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RESULT 1 US-08-810-572A-6 US-08-810-572A-6 Sequence 6, Application US/08810572A Patent No. 50612 GREERL INFORMATION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS TITLE OF INVENTION: THEROPY SURFACE RECEPTOR THE SAME AND ME TITLE OF INVENTION: THEROPY SURFACE OF INVENTION: THEROPY SURFACE RECEPTOR THE SAME AND ME TITLE OF INVENTION: THEROPY SURFACE RECEPTOR THE SAME AND ME TITLE OF INVENTION: THEROPY SURFACE RECEPTOR THE SAME AND ME TITLE OF INVENTION: THEROPY SURFACE RECEPTOR THE SAME AND ME TITLE OF INVENTION: THEROPY SURFACE RECEPTOR THE SAME AND ME SURFACE SURFACE RECEPTOR THE SURFACE FORM. CURTURE READABLE FORM. LEGISTATION SURFACE PORM. MEDIUM TYPE: Ploopy disk COMPATION: USA CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/810,572A CURRENT APPLICATION DATA: APPLICATION SURFACE S	28 53.5 22.4 77 2 US-08-486-399-4 Sequence 4 29 53.5 22.4 77 2 US-08-486-399-40 Sequence 4 30 53.5 22.4 77 2 US-08-461-965-4 31 53.5 22.4 77 2 US-08-461-965-40 Sequence 4 32 53.5 22.4 77 2 US-08-326-110A-33 Sequence 3 33 53.5 22.4 77 2 US-08-634-641-40 Sequence 4 34 53.5 22.4 77 2 US-08-634-641-40 Sequence 4 35 53.5 22.4 77 3 US-09-249-471-40 Sequence 4 36 53.5 22.4 77 3 US-09-249-471-40 Sequence 4 37 53.5 22.4 77 3 US-09-249-472-4 Sequence 4 38 53.5 22.4 77 3 US-09-249-451-40 Sequence 4 40 53.5 22.4 77 3 US-09-249-451-40 Sequence 4 40 53.5 22.4 77 3 US-09-249-451-40 Sequence 4 41 53.5 22.4 77 3 US-09-249-451-40 Sequence 4 42 53.5 22.4 77 3 US-09-249-451-40 Sequence 4 43 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 44 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 45 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 45 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 46 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 47 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 48 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 49 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 49 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 40 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 40 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 41 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 42 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 43 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 44 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 45 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 46 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 47 53.5 22.4 77 3 US-09-249-461-40 Sequence 4 48 53.5 22.4 77 3 US-09-249-461-40 Sequence 4
D METHODS OF USE	

28.2%;

Score 67.5; DB Pred. No. 0.61;

Length 166

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US-09-290-333-6
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                                                                                                      RESULT 3
US-08-810-572A-2
                                                                                                                                                                                                                                                                                                                      US-09-290-333-6
Sequence 2, Application US/08810572A
Patent NO. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application Patent No. 6316222 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                          5 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-199
CLASSIFICATION: CUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 26,742
REFERENCE_DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
STREET: 411 Hackensack Ave,
                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptid HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bram,
                                                                                                                                                                             CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 68
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CANT: VON Bulow, Gotz
OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floor
                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                               28.2%; Score 67.5; DB 30.6%; Pred. No. 0.61; Live 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Richard J.
ulow, Gotz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/09290333
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THEREOF
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                                                                                                                                                                                                                                                                                                                                      6:
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Continental Plaza,
                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                Length 166;
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                                                                                                                                                                                                                                                 Gaps
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US-09-290-333-2
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                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09290333 Patent No. 6316222 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11:
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CAML, NUCLE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acid
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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MEDIUM TYPE: Floppy disk
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STREET: Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA 40
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                CORRESPONDENCE ADDRESS: David A. Jackson,
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
                                                                                                                                                                                                                                                                                                                          APPLICANT: Bram,
                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 30.6
11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                          CITY: Hackensack
STATE: New Jersey
                                                                                                           COUNTRY:
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                                                                                          ZIP: 07601
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30.6%;
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Pred. No. 1.1;
9; Mismatches
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                                                                                                                                                                               Continental Plaza,
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   Version #1.30
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333

FILING DATE: 12-Apr-1999 CLASSIFICATION: <Unknown>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2,
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                                                                 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                           SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino aci
                                                                                                                   REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of TITLE OF INVENTION: Sperm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P. O. CITY: Houston STATE: Texas
                                                                    TELEFAX: /1.
TELEFAX: 79-0924
                                                                                   TELEPHONE: 713-789-2679
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                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/276,90 FILING DATE: Submitted Herewith
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                77210-4433
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
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                              2476 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arnold, White & Durkee
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                                                                                                                                                                                                                                                             US/08/276,967
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Pred. No. 1.
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US-08-718-388-9
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                                                                                                                                                   RESULT 7
                                                                                                  Sequence 4, Application US/08999811 Patent No. 5932540
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Best Local Similarity
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ZIP: 22040-074,

COMPUTER READABLE FORM:

COMPUTER: FLOPPY disk

MEDDIUM TYPE: Floppy disk

MEDDIUM TYPE: TBM PC compatible

""GTEM: PC-DOS/MS-DOS

""GTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 205-805
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                   GENERAL INFORMATION:
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APPLICANT: HU, JING-
APPLICANT: ROSEN, FR
APPLICANT: CAO, LIAN
TITLE OF INVENTION: '
                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1851 CSAHSYYTSCVPSCLPSCQDPEGQCTGAGAPSTCEEGC 1888
                                                                                                                                                                                                   3933 ECPQNSHYE----LCADTCSLGCSALSAPLQCPDGC 3964
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APPLICANT: HARADA, NAOKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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CITY: FALLS CHURCH
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nes 12; Conserv
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                                                                                                                                                                                                                                4 QCSQNEYFDSLLHACI-PCQLRCSSNTPPLTCQRYC 38
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                 5405 amino acids
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                                   LIANG
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31.6%;
                                                  CRAIG A.
                                                                                                                                                                                                                                                                              23.2%;
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     VASCULAR ENDOTHELIAL GROWTH FACTOR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                              Score 55.5; DB 4;
Pred. No. 4.7e+02;
6: Mismatches 13;
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Pred. No. 1.9e+02;
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CORRESPONDENCE ADDRESS:

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NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: HOMO Sapiens
US-08-824-996-2
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US-08-824-996-2
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Patent No. 5935820
                              Query Match
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Matches
                Best Local
                                                                                                                                                                                                                                          APPLICANT: Rosen, Graig A.
APPLICANT: Cao, Liang
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Factor 2
                                                                                                                                                                                                           FILE REFERENCE: PF112D1
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             EARLIER APPLICATION NUMBER: 08/207,550 EARLIER FILING DATE: 1994-03-08
                                                                                                                                                                                                                                                                                                     APPLICANT: Hu, Jing-Shan
APPLICANT: Rosen, Craig A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 01
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 06-JUN-1995
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 1488.1000004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Similarity 35.0%;
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Conservative
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35.0%;
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                              Score 54.5;
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Pred. No. 41;
                Pred. No.
Mismatches
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RESULT 10
US-08-510-133A-33
; Sequence 33, Application US/08510133A
; Patent NO. 6221899
; GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
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US-09-042-105-4
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GENERAL INFORMATION:
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                                                                                                                                                                                           Matches
                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
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APPLICANT:
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CORRESPONDENCE ADDRESS: ADDRESS: STEPONT
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COMMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
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                                                                                                                                     258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES
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CLASSIFICATION:
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CLASSIFICATION:
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14; Conserv
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ON:
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/08585895
Patent No. 6245530
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Best Local S
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
                                                                                          SOFTWARE: PatentIn Relu
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                  ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 296
                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                    FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                           CITY: Chicago
                                                                                                                                                                                                                                                                        STATE:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                  COUNTRY: United States of America
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Receptor Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 41
                                                                                                                                                                                                                                  60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/510,133A FILING DATE: 01-Aug-1995 CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America ZIP: 60606-6402
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gass, David A. REGISTRATION NUMBER: 38,153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                    Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 350 amino acids
                                                                                                                                                                                                                                                                                                         E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
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35.0%;
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38,153
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Pred. No. 41;
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                                                         ; MOLECULE TYPE: US-08-999-811-2
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                            Query Match
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               Best Local Similarity
                                                                                                                                             TELEFAX: (202)371-254 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acid
TYPE: amino acid
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acid
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US FILING DATE: 8-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MPDIUM TYPE: Floppy disk
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ADDRESSEE: STERNE, KESSLER, CONTREET: 1100 NEW YORK AVENUE
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TELEFAX: 25-3856
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                                                                                    TYPE: amino acid TOPOLOGY: linear
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CLASSIFICATION:
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                                                                                                                                                                                                                                    NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
 14;
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                                                                                                                                                                                                                               MARKOWICZ, KAREN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08999811
                                                                                                               419 amino acids
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                                                                                                                                                          (202)371-2540
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 Conservative
                                                                                                                                                                        202)371-2600
                                                                     protein
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35.0%;
               22.8%;
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                                                                                                                                                                                                                                                                           US 08/465,968
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               Pred. No.
                           Score 54.5;
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Pred. No. 41;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
               49
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                            DB 2;
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                         Length 419;
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Indels
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Matches

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QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS

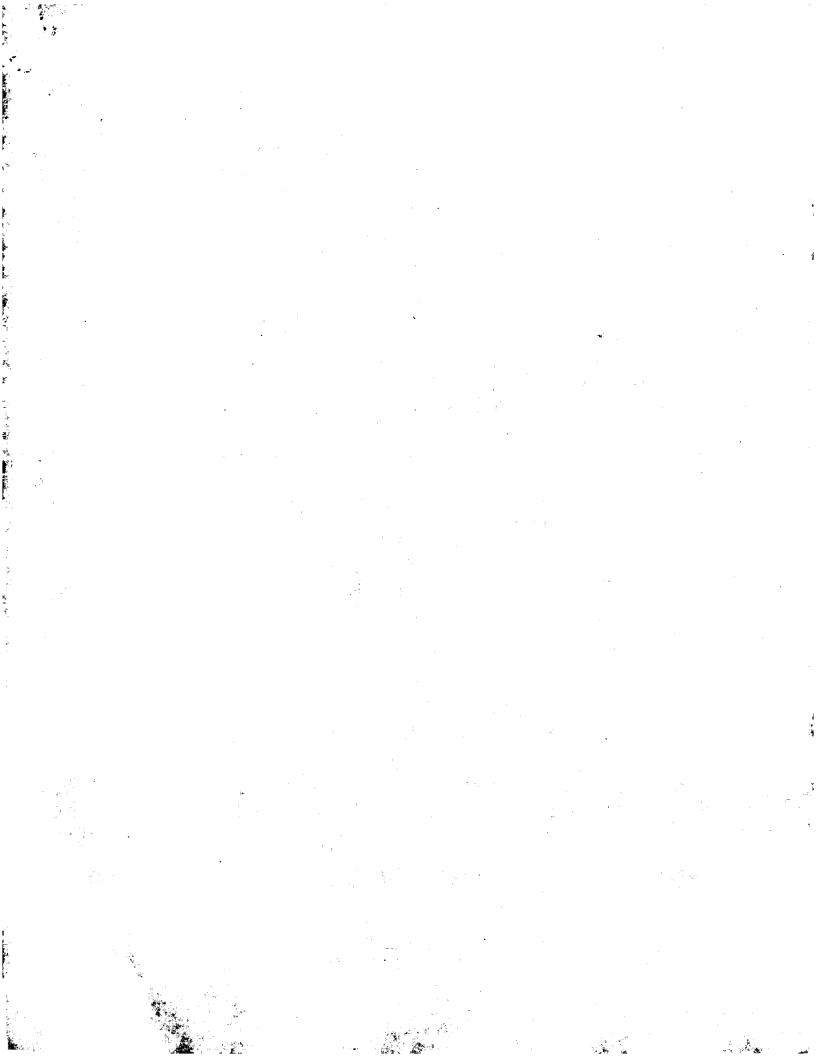
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327

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RESULT 14
US-09-042-105-18
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Sequence 18, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09042105
Patent No. 6040157
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HU, JI
                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: LLUC
CITY: WASHINGTON
STATE: DC
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CORRESPONDENCE ADDRESS: STERET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                              327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: HEREW CLASSIFICATION:
                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/207,550 FILING DATE: 8-MAR-1994
                                                                                                                                                                                                               Local
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CAO, LIANG
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US-08-795-430-8
                                                                                                                                                                                            Sequence 8, Application US/08795430 Patent No. 6130071
                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Alitalo,
APPLICANT: Joukov,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)371-254 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: US 08/465,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                             APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 57
                                                                            CORRESPONDENCE ADDRESS:
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                                CITY: Chicago
                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
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                                                           ADDRESSEE:
 COUNTRY:
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6300 Sears Tower,
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States of America
                                                                                             Vascular Endothelial Growth Factor
Protein and Gene, Mutants Thereof,
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fower, 233
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Pred. No. 49;
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South Wacker Drive
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Search completed: November 12, 2002, 17:01:42 Job time: 6.76824 secs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-630
TELEPAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                        Query Match 22.8
Best Local Similarity 35.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/F196/0042
FILING DATE: 01-AUG-1996
PRIOR APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION NUMBER: 08/501,132
FILING DATE: 12-JAN-1996
PRIOR APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVId A.
RECISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28,967.73
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
                                                                                   327 QCGANREPDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
                                                                                                                           4 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 41
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
j /cgn2_6/ptodata/1/pubpaa/US97_NEW_PUB.pep:*
j /cgn2_6/ptodata/1/pubpaa/US97_PUBCOMB.pep:*
j /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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j /cgn2_6/ptodata/1/pubpaa/US99_PUBCOMB.pep:*
j /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
j /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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j /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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US-09-854-864-5
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Sequence 6, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 21, Appli
Sequence 13, Appli
Sequence 11, Appli
Sequence 10, Appli
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Sequence 20, Appli
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Sequence 41, Appli
Sequence 42, Appli
Sequence 42, Appli
Sequence 42, Appli
Sequence 22, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 18, Appli
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51	51	51	51	51	51	51	51.5	51.5	51.5	52	53	54.5	54.5	54.5	54.5	55.5	56	59	59.5	59.5	64.5	64.5	64.5	64.5	64.5
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Sequence 9, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 12, Appl	Sequence 4, Appli	Sequence 3, Appli		Sequence 39, Appl			Sequence 61, Appl	Sequence 3, Appli	Sequence 2, Appli	Sequence 22, Appl	Sequence 3, Appli	Sequence 1116, Ap	Sequence 10, Appl	Sequence 46, Appl	•	Sequence 25, Appl	16,	Sequence 14, Appl		Sequence 10, Appl	Sequence 2, Appli

ALIGNMENTS

RESULT 1 US-09-854-864-6

; Sequence 6, Application US/09854864; Patent No. US20020081296A1

GENERAL INFORMATION:

OF MATTER CONCERNING APRIL/G70, BCMA

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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 6
GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: TUT, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA

TITLE OF INVENTION: BLYS/AGP-3, AND TACI
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                                                                                                                      ; Sequence 5, Application US/09B54B64
; Patent No. US200200B1296A1
                                                                                                                                                                  RESULT 2
US-09-854-864-5
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Best Local S
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TYPE: PRT
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Local Similarity 100.0%; Pred. No. 3.2e-22;
hes 42; Conservative 0; Mismatches 0;
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
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; ORGANISM: Homo sapiens
US-09-854-864-9
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CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                              US-09-854-864-21
                                                                                                                                                                                                                                         Sequence 21, Application US/09854864 Patent No. US20020081296A1 GENERAL INFORMATION:
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Best Local
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LENGTH: 283
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
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PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
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FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
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US-09-854-864-7
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US-09-854-864-13
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APPLICANT: THEILL,
APPLICANT: YU, GAN
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APPLICANT: THEILL,
APPLICANT: YU, GAN
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Best Local Similarity
Matches 38; Conserv
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LENGTH: 58
                                                                                SEQ ID NO 13
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ORGANISM: Consensus -09-854-864-13
                                                                                                                      PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
                                                                                                                                                                                                                                                                  FILE REFERENCE: A-686B
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                                                                                                   SOFTWARE: PatentIn version 3.1
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TYPE: PRT
ORGANISM: Homo sapiens
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ilarity 100.0%;
Conservative (
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Pred. No. 8.4e-20;
0; Mismatches 0;
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APPLICANT: THEILL, LARS EYDE

APPLICANT: YU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27
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                                                                                                                         ; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09854864 Patent No. US20020081296A1 GENERAL INFORMATION:
                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1 SEQ ID NO 10
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Best Local
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                                                                                    Query Match
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
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                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 3:
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nes 29; Conservative
                                                     Local Similarity
mes 29; Conserv
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1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
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34; Conserv
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                                                     Conservative
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Pred. No.
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Pred. No. 7e-12;
                                                                   Score 156; DB 10; Length 281; Pred. No. 1e-11;
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1.5e-17;
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; Sequence 20, Application US/09854864
; Patent No. US20020081296A1
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US-09-854-864-12
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US-09-779-050A-45
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SEQ ID NO 12
LENGTH: 117
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GENERAL INFORMATION:
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LENGTH: 37
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Best Local :
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Best Local Similarity 30.6%;
Matches 11; Conservative
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APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF FILING DATE: 2000-02-11
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SOFTWARE: PatentIn version 3.0
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ORGANISM: Homo sapiens
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Local Similarity 63.9%;
es 23; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
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Pred. No. 6.4e-05;
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APPLICANT:

THEILL, LARS EYDE YU, GANG

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RESULT 13
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
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US-09-854-864-15
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Best Local S
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LENGTH: 59
TYPE: PRT
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Patent No. US20020081296A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 60/181,800 PRIOR FILING DATE: 2000-02-11 NUMBER OF SEQ ID NOS: 52
                                                      CURRENT APPLICATION NUMBER: US/09/779,050A CURRENT FILING DATE: 2001-02-12
                                                                                          APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
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TYPE: PRT
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; ORGANISM: Homo sapiens 
US-09-779-050A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/09879919 Patent No. US20020064829A1
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CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-24
PRIOR PILING DATE: 2001-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/779,050A CURRENT FILING DATE: 2001-02-12 PRIOR APPLICATION NUMBER: 60/181,800 PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
                                                                                                                                                                     PRIOR FILING DATE: 2001-03-16 PRIOR APPLICATION NUMBER: 60/254,875
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yu, Guo-Liang, et al. TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon FILE REFERENCE: PF253P1
                                                                         PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 52
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PRIOR APPLICATION NUMBER: 60/016,812 PRIOR FILING DATE: 1996-03-14
                                                                                                                                                     PRIOR FILING DATE: 2000-12-13
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TYPE: PRT
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622.203 Million cell updates/sec
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hypothetical prote
gibberellin-regula
zonadhesin - pig
hypothetical prote
myosin heavy chain
myosin-IXb [simila
hypothetical prote
finger protein YJL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                chymotrypsin/elast hypothetical prote furin (EC 3.4.21.7
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hypothetical prote
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furin (EC 3.4.21.7
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
52	52	52	52	52	52	52	52.5	52.5	52.5	53	53	53	53	53.5	53.5
21.8	21.8	21.8	21.8	21.8	21.8	21.8	22.0	22.0	22.0	22.2	22.2	22.2	22.2	22.4	22.4
1483	1474	1077	689	547	304	56	847	389	118	596	592	294	274	927	915
N	N	N	N	N	μ.	2	N	N	2	2		N	ผ	N	Ν
S30015	D88550	T41146	T52060	T34318	JC2264	JN0380	D72860	T29488	S61051	F88188	JC1480	T23682	FB6276	T21772	T21773
hypothetical prote	protein ZC84.6 [im	probable cysteine-	protein MEDEA [imp	hypothetical prote	tissue factor path	trypsin inhibitor	viral capsid assoc	hypothetical prote	hypothetical prote	protein C18H9.7 [i	protein kinase C (hypothetical prote	F14L17.2 protein -	hypothetical prote	hypothetical prote

ALIGNMENTS

RESULT S43486

B-cell maturation factor - human N;Alternate names: BCM protein; BCMA protein; BEL protein

C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C;Accession: \$43486; \$31208; \$36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, A;Reference number: \$43486; MUID:94218235; PMID:8165126
A;Accession: \$43486

is bic

A;Status: preliminary A;Molecule type: DNA

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RESULT 2
$34.583
$34.583

Safetine proteinase (EC 3.4.21.-) PC6B - mouse serine proteinase (EC 3.4.21.-) PC6B - mouse (;Species: Mus musculus (house mouse) C;Pate: 02-Dec-1993 #sequence_revision 10-Nov C;Pate: 02-Dec-1993 #sequence_revision 10-Dec-1993 #sequence_revision 10-Dec-1993 #sequence_revi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-184 <LAA>
A; Residues: 1-184 <LAA>
A; Residues: 1-184 <LAA>
A; Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245
A; Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245
R; Laabl, Y; Grass, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapiembo J. 11, 3897-3904, 1992
A; Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(A; Reference number: S31208; MUID:93010984; PMID:1396583
A; Accession: S31208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: GDB:BCMA
A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor
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A; Residues: 4-184 <LA3>
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A; Residues: 1-184 <LA2>
A; Cross: references: EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PID:g29408
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Best Local
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Pred. No. 1.1e-20;
; Mismatches 0;
                                                                                                                            10-Nov-1995 #text_change 05-Nov-1999
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RESULT 4
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J. Biol. Chem. 273, 3415-3421, 1998
A;Title: Species diversity in the structure of zonadhesin,
A;Reference number: Z22080; MUID:98123114; PMID:9452463
A;Accession: T42215
                                                    A; Status, Frank
A; Molecule type: DNA
A; Residues: 1-1101 <GEI>
A; Cross-references: EMBL: U39644; NID: g1049339; PID: g1049343; PIDN: AAA80360.1;
A; Cross-references: EMBL: U39644; NID: g1049339; PID: g1049343; PIDN: AAA80360.1;
                                                                                                                                                                                                                                               hypothetical protein T10E10.4 - C.C; Species: Caenorhabditis elegans C; Date: 20-Sep-1999 #sequence_rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: sperm-specific membrane protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec.1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T42215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 327, 165-171, 1993
A; Title: Identification of an isoform with
A; Reference number: S34583; MUID: 93327934;
                                                                                                                                                    submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid
A;Reference number: 218588
A;Accession: T16840
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C; Function:
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A; Residues: 1-5376 <G
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:Cross-references: GB:D17583; NID:9407344; PIDN:BAA04507.1;
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                                               CESP: T10E10.4
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    Match
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14; Conserv
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                                 152/2;
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                                 191/3; 209/2; 283/3;
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   27
 . 68;
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Pred. No. 2.8;
5; Mismatches
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Pred. No.
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 66;
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Length 1101;
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                                 465/1;
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                                 RESULT
T25169
 hypothetical C; Species: C:
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C;Keywords: transmembrane protein F;1-26/Domain: signal sequence #status predicted F;27-3034/Product: seven-pass transmembrane recep
                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, Octob A; Description: The Celsr family of novel
                                                                                                                                                                                                                                                                                                                                                              seven pass transmembrane receptor protein precursor - C:Species: Mus musculus (house mouse) C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te C:Accession: T14119
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A;Cross-references: EMBL:Z68888; NID:g1167859;
A;Experimental source: clone Sfurin 6; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: Z22368
A; Accession: T43251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        furin (EC 3.4.21.75) - fall armyworm N,Alternate names: paired basic amino acid cleaving enzyme; proprotein conv C;Species: Spodoptera frugiperda (fall armyworm) C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
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A; Residues: 1-3034 <HAD>
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                                                                                                                                                                                                                                                                                                                                   R;Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R. submitted to the EMBL Data Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated
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                                                                                                                                                                                        A;Gene: Celsrl
                                                                                                                                                                                                                    A;Cross-references: EMBL:AF031572; NID:g3800735; PID:g3800736; PIDN:AAC68836.1
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Matches
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                             4 OCSONEYFDSLLHACIPCQL-----RCSSNTPPLTCQ----
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7; Mismatches
                                                                            Score 59.5;
Pred. No. 71;
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Caenorhabditis

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Caenorhabditis

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submitted to the EMBL Data Library, October 1996
A; Reference number: Z19990
A; Accession: T25169
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-330 < WILL
A; Residues: 1-330 < WILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C23G10.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 *te:C;Date: 20-Sep-1999 *te:C;Accession: T15577 R;Latreille, P. R;Latreille, P. Submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid C23G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25169
R;Wilkinson, J.
                                                                                                                                                                                                                                                                                                                              epidermal growth factor receptor homolog precursor - fluke (Schi K;Contains: protein-tyrosine kinase (EC 2.7.1.112) C;Species: Schistcosoma mansoni C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C;Accession: A4558; S27836 R;Shoemaker, C.B.; Ranachandran, H.; Landa, A.; dos Reis, M.G.; Mol. Blochem. Parasitol. 53, 17-32, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:C23G10.8
A;Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
C;Superfamily: Caenorhabditis elegans hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-758 <LAT>
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1717 <a href="https://docume.nlm.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.ops.nih.gold.
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A; Accession: T15577
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Pred. No.
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Pred. No. 25;
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RESULT A43434

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Arch. Blochem. Biophys. 232, 143-161, 1984
A. Title: The isoinhibitors of chymotrypsin/elastase from Ascaris
A. Reference number: S07127; MUID:84255715; PMID:6564898
A. Accession: S07127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SER (Symperfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homolog; Superfamily: fluke epidermal growth factor receptor homolog; protein; phosphoprot C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprot F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>F;1018-1323/Domain: protein kinase homology <KIN>F;1026-1034/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
T23681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Ascaris lumbricoides (common roundworm)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997
C;Accession: S07127
R;Babin, D.R.; Peanasky, R.J.; Goos, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein M02G9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #t.C;Accession: T23681
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                                                                                                                                                    A; Map position: 3
A; Introns: 23/3;
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A; Residues: 1-1513 <WIL>
                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T23681
                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, A; Reference number: Z19781
                                                                                                                                                                                                                                                                                                                                                                                             R; Matthews, L.
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                                                                                                                                                                                             A; Gene: CESP: M02G9.1
                                                                                                                                                                                                                                  A; Experimental source: clone M02G9
                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z81573; PIDN:CAB04625.1; GSPDB:GN00020; CESP:M02G9.1
                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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DSCQNVCQNVCQGACVSQNSPPAVCQQTCRQS
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                                                                                             Similarity
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36.6%;
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                                                                                           Score 58; DB Pred. No. 59;
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Pred. No. 50;
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172
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hypothetical protein T23K8.9 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: G96675 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Hulzar, L.
                                                                                                                                                                                                                                                                                        RESULT
G96675
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T20130
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C;Superfamily: subtilisin homology
C;Keywords: hydrolase; serine proteinase; transmembrane pro
F;409-652/Domain: subtilisin homology <SBT>
F;418,457,638/Active site: Asp, His, Ser #status predicted
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A;Accession: A43434
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, B16-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C50H2.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C;Speciles: Drosophila melanogaster
C;Date: 04-Mar-1993 *sequence_revision 18-Nov-1994 *text_char
C;Accession: A43434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 5
A; Introns: 72/1; 122/1; 152/3; 188/1; 209/1; 255/1; 301/1; 339/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-502 <WIL>
A; Cross-references: EMBL: 273971; PIDN: CAA98256.1; GSPDB: GN00023; CESP: C50H2.3b
A; Experimental source: clone C50H2
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A; Accession: T20130
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R; McMurray, A.
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A;Residues: 1-1680 <ROE>
A;Cross-references: GB:M94375; NID:g157461; PID:g157462
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
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17; Conserv
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34.3%;
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Pred. No. 74;
5; Mismatches
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                                 Khaykin, E.; Kim, C
Maiti, R.; Marziali,
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Search completed: November Job time: 8.48927 secs

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RESULT 15
T20125
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A;Residues: 1-838 <WIL>
A;Cross-references: EMBL:273971; PIDN:CAA98251.1; GSPDB:GN00023; CESP:C50H2.3a
                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20125
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A;Molecule type: DNA
A;Residues: 1-653 <STO>
                                                                                                                                                           A; Introns: 31/1;
                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data A; Reference number: Z19226
                                                                                                                                                                                                                                                                                                                                                                                                         R; McMurray, A.
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                                                                                                                                                                                                                                        A; Experimental source: clone C50H2
                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: T20125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C50H2.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
                                                                                                                                                                                                  A;Gene: CESP:C50H2.3a
                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                       1 MAGQCSQNEYFDSLLHACIPCQL----RCSSNT-----PPLTCQRYCNA 40
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O35161 mus musculu
P07851 ascaris suu
P30432 drosophila
O9ulto homo sapien
P46687 arabidopsis
O28983 sus scrofa
P42124 drosophila
P49767 homo sapien
O63358 rattus norv
O99706 mus musculu
O13459 homo sapien
O29537 canis famil
P39529 saccharomyc
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Nature 404:995-999(2000).
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Harrison K., Kindsvogel W., Clegg C.H.;
"TACI and BCMA are receptors for a TNF homolo
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J. Immunol. 165:1322-1330(2000).
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C. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).

FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.

Promotes B-cell survival and plays a role in the regulation humoral immunity. Activates NF kappa-B and JNK.

SUBUNIT: ASSOCIAtes with TRAFI, TRAF2, TRAF3, TRAF5 and TRAF SUBCELLULAR LOCATION: Type III membrane protein. Plasma memb and perinuclear Golgi-like structures.

TISSUE SPECIFICITY: Expressed in mature B-cells, but not in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.-B., Johnson H.;
                                                                                                                                                                                                                                                                                                             $31208; $31208.
$31209; $31209.
$4 HGNC:11913; TNFRSF17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHICH INVOLVES BCMA AND IL2. SIMILARITY: CONTAINS 1 THER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZED BY A CHROMOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells or monocytes.
DISEASE: A FORM OF T-CELL
                                                                                                                                                                                                                                                                                                                                                                  AB052772; BAB60895.1;
S31208; S31208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K., Xu W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *20259066; PubMed=10801128; Enselman R., A., Johnston J., Mudri S., Enselman R., K., Xu W., Parrish-Novak J., Foster D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                maturation protein is a receptor for the tumor necrosis
                                                                                                                                                                                                                                                                                       Immune response;
  184
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24
28
153
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7
  ξ,
                                                                                                                                                                                                                                                                    Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRAF5
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PubMed=10908663;
                                        184
41
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153
  20138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TNFR-CYS REPEAT.
  ¥
                                                                                                                                                                                                                    translocation; Polymorphism.
EXTRACELLULAR (POTENTIAL).
SIGNAL ANCHOR (TYPE III MEMBRANE
                                                                                                                                                                                                                                                                  Proto-oncogene; Signal-anchor;
translocation; Polymorphism.
                                      BREAKPOINT FOR TRANSLOCATION T
INTERLEUKIN 2/BCM ONCOGENE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                               (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
TNFR-CYS.
  /FTId=VAR_012234.
277AF11E2767D932 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSLOCATION 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T(4;16)(Q26;P13)
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Blumberg
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RA AIZAWA K., IZAWA M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA AIZAWA K., IZAWA M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boitelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,
RA Nacaski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sazaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashina J., Masegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TR17_MOUSE 088472;
                                                                           -!- SUBUNIT: ASSOCIATES WITH TRAFT, TRAF2, TH
SIMILILIUAR LOCATION: Type III membrane produced by alternative splicing.
produced by alternative splicing.
!- TISSUE SPECIFICITY: Detected in spleen, theart, and at lower levels in kidney and elsewing similarity: CONTAINS 1 TNFR-CYS REPEAT.
                                                                                                                                                                                                                                            "Functional annotation o
Nature 409:685-690(2001)
-1- FUNCTION: Receptor f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J; TISSUE-Colon; MEDLINE-21085660; PubMed-11217851; Kawai J., Shinagawa A., Shibata K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Madry C., Laabi Y., Callebaut I., Roussel J., Hatz
Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
"The characterization of murine BOMA gene defines
of the tumor necrosis factor receptor superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002
15-JUN-2002
15-JUN-2002
 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C; TI:
MEDLINE-99061155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maturation protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor necrosis factor receptor
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFRSF17 OR BCMA OR BCM
                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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European
by non-
                                                                                                                                                                                            FUNCTION: Receptor for INFSF13B/BLYS/BAFF and INFSF13/APRIL. Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and JNK (By similarity) SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol.
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42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel.
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               Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Spleen;
5; PubMed-9846698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Pred. No. le-
D; Mismatches
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otation update)
superfamily member 17
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 long
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superfamily.";
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                restrictions
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Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Klyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli P., Buruno M., Aono H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubli P., Buruno M., Aono H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubli P., But C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki-H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 13B
activator and CAML interactor).
TNFRSF13B OR TACI.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T13X_MOUSE
Q9ET35; Q9I
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Dixit V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-Lung; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               humoral immunity
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MEDLINE-21177254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSV 40
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29; Conservative
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S.A., Grewal I.S.,
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CYTOPLASMIC (POTENTIAL).

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Pred. No. 1.7e-12;
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Sciurognathi; Muridae
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Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.
"TACI-ligand interactions are required for T
collagen-induced arthritis in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20341628; PubMed=10880535; Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boon Theill L.E., Colombero A., Solovyev I., Lee F., McC Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wa Meng S.-Y., Boyle W.J., Hsu H.; "TACI is a TRAF interacting receptor for TALL-1, a fold of the state of the state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
[3]
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"Functional
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FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type III membrane SIMILARITY: CONTAINS 2 THER-CYS REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMLG with its C-terminus (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
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                                     CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC
CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC
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TNER_NGFR_2; 2.

TNER_NGFR_2; 2.

response; Signal-anchor; Transmembrane; Repeat.
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EXTRACELLULAR (POTENTIAL).

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*TGNAL-ANCHOR (TYPE III MEMBRANE PF
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CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 2.
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.S.;
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                                                                                                                                                            CRC64;
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., Elliott R.,
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RESULT 4
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Q04592; Q62040; Q1-FEB-1995 (Rel. 31, Created) Q1-FEB-1995 (Rel. 40, Last sequence update) 15-JUN-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-) (Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (Convertase PC5) (Subtilisin-like proprotein convertase 6)
                                                                                                                                                                                                                                                                                                              MEDLINE-97436919; PubMed-9291583;
Rancourt S.L., Rancourt D.E.;
"Murine subtilisin-like proteinase SPC6 is expressed during implantation, somicogenesis, and skeletal formation.";
Dev. Genet. 21:75-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96293359; PubMed=8698813;
Constam D.B., Calfon M., Robertson E.J.;
"SPC4, SPC6, and the novel protease SPC7
morphogenetic proteins at distinct sites
J. Cell Biol. 134:181-191(1996).
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J. Cell Biol. 135:1261-1275(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                candidate proprotein nonendocrine cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM PC5A).
TISSUE-Brain, and intestine;
MEDILINE-93224489; Pubmed-8468318;
Nakagawa T., Hosaka M., Torii S.,
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STRAIN-ICR; TISSUE-Intestine;
MEDLINE-93327934; PubMed-8335106;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Bie I., Marcinkiewicz M., Malide D., Bendayan M., Seidah N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION MEDLINE-97103178; PubMed-8947550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah "cDNA structure of the mouse and rat subtilisin/kexin-like PC candidate proprotein convertase expressed in endocrine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Adrenal cortex; MEDLINE-93342056; PubMed-8341687;
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"Identification of an isoform with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCSK5
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PUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE FOR THE MATURATION OF GASTROINVESTINAL PETTIDES. MAY BE INVOLVED IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATIO OF GROWTH FACTORS.

CAPALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPROTEINS BY CLEAVAGE OF ARC-XAA-YAA-ARC-|-ZAA BONDS, WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.

SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ayan M., Seidah N.G.;
isoforms of proprotein convertase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natl. Acad.
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Metazoa; Chordata; C
Metazoa; Rodentia; દ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sci.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are coexpressed with bone
during embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are sorted to different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T., Murakami K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.,
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                                                                                                                                                                                                                                                                                                                                                                            embryonic
                                                                                                                                                                           ACTIVATION
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              A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT I EARLY ENDOSOMES.
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PCS AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SET TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST
                                                          ISOFORMS; PC5B/LONG
                                                                                                  Ħ
                  TISSUES
                                                                                                  COMMUNICATION WITH
                                                        (SHOWN
                  BUT
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ABUNDANT IN THE INTESTINE AND ADRIALS, PCSB IS EXPRESSED IN THE INTESTINE, ADRINALS AND LUNG BUT NOT IN THE BRAIN.

1. DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO, EXCEPT IN THE DEVELOPING MERVOUS SYSTEM, THE RIBS AND THE LIVER, BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENCIATED DECIDIA. AT E7.5, INVENSE EXPRESSION IN EXTRABBRYONIC ENDODERM, AMNION AND NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK SAC FOLLOWED BY A CONFINATION TO DERMANYOTOME COMPARTMENT. BETWEEN E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED TO THE COMDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS STAGE, STRONG EXPRESSION AND IN THE MUSCLE OF THE TONGUE. AT E16.5, ABUNDANT EXPRESSION TO THE COMPANIA EXPRESSION TO THE COMPANIA THE MUSCLE OF THE INTESTINAL VILLI. ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF ISOFORM B OCCUR AT E12.5.

1. DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC CRUTICUM.

2. DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN SORTING TOPPORATION. AC 1 DIRECTS TON LOCALIZATION AND INTERACTS.

DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACID) SORTING INFORMATION. AC 1 DIRECTS TON LC WITH THE TGN SORTING PROTEIN PAGS-1. SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.

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EMBL; D17583; BAA04507.1; -
EMBL; D12619; BAA02143.1; -
EMBL; D14932; AA074636.1; -
PIR; JX0248; JX0248.
PIR; A48225; A48225.
  DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                              SIGNAL
PROPEP
CHAIN
                                                                                                               PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P. domain; 1.
SMART; SM00181; EGF; 3.
SMART; SM00001; EGF_Like; 2.
SMART; SM00261; FU; 22.
                                                                    Cleavage on pa
Transmembrane
                                                                                          PROSITE; PS00136;
PROSITE; PS00137;
PROSITE; PS00138;
                                                                                                                                                          InterPro; IPR000561; EGF-like.
InterPro; IPR002174; Furin-like.
InterPro; IPR002884; P_domain.
InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 1.
                                                                                                                                                                                               MEROPS; S08.076; -. MGD; MGI:97515; Pcsk5
                                                                                                                                                                                                               HSSP;
                                                                                    Hydrolase;
                                                                                                                                                    PF01483; P;
                                                                                                                                                                                                              099405;
   117
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1790
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                                                                                    Serine
                                                                           pair
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                                                                          ; SUBTILASE_ASP; 1.
; SUBTILASE_HIS; 1.
; SUBTILASE_EIST; 1.
; SUBTILASE_SER; 1.
e protease; Glycoprotein; Zymogen; Signa of basic residues; Repeat; Alternative
   1768
1789
1877
452
602
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116
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                                                                                                                                                     PARTIAL.
TYPE 5.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CATALYTIC.
HOMO B.
                                              PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
                                                                                   Signal;
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RESULT 5
ZAN_MOUSE
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Best Local
  Gao Z., Harumi T., Garbers D.L.;

"Chromosome localization of the mouse zonadhesin gene (ZAN)";

Genomics 41:119-122(1997).

-i- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITIC SIGNALING.

-i- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

-i- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

-i- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

-i- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPPING TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPPING THE SPERM HEAD.
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                       ZAN_MOUSE STANDARD: PRT; 53/6 AA. 088799; 008647; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
SEQUENCE
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CARBOHYD
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CARBOHYD
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Mammalia; Eutheria;
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                                                                                                                                             TISSUE=Testis;
MEDLINE~97271566; PubMed=9126492;
                                                                                                                                                                                                             domains.
                                                                                                                                                                                                                         membrane protein
                                                                                                                                                                                                                                                      Gao Z.,
                                                                                                                                                                                                                                                                MEDLINE=98123114;
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                   Zonadhesin precursor
                                                                                                                                                                         SEQUENCE OF 4864-5376 FROM N.A.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                           Species diversity in the structure of zonadhesin, membrane protein containing multiple cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 QCSQNEYFDSLLHACIPCQLRCSSNTPP-----LTCQR 36
                                                                                                                                                                                                   Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                    Garbers
                                                                                                                                                                                                   Chem.
                                                                                                                                                                                                                                                                                                                    ıs (Mouse).
Metazoa; Chordata; C
™+heria; Rodentia; {
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1856
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AA; 209287
                                                                                                                                                                                                                                                                PubMed=9452463;
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523
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804
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      IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS
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AC 1.
AC 2.
CLEAVAGE (AUTO-) (BY S
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CHARGE
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69.5;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EC850E2DF20EA1C3
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DF20EA1C3 CRC64;
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                              PROTEIN,
                                                                    MANNER TO THE RECOGNITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                     gene
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                                                                                                                                                                                                                           a sperm-specific molecule-like
                              EXCLUSIVELY ON
                                                                    ON AND/OR
                                                                                                                                                                                                                                                                                                                                Murinae;
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                                                                                                                      the
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                                                                                PELLUCIDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.
      -!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
SPERMAFOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
-!- DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT
OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
-!- SIMILARITY: CONTAINS 3 MAM DOMAINS.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
    DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
SMART;
SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contitles requires a license.
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                                                                                                                                                                                                                                                                                                                                                                       Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00022; EGF_1;
PROSITE; PS01186; EGF_2;
PROSITE; PS00740; MAM_1;
PROSITE; PS50060; MAM_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:106656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U97068; AAC26680.1; -. EMBL; U83190; AAC53125.1; -.
                                                                                                                                                                                                                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                              Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZONA PELLUCIDA.
DOMAIN: DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PF00629; MAM; 3.
; PF01826; TIL; 25.
; PF02345; TILa; 25.
T; SM00181; EGF; 2.
T; SM00274; FOLN; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r; PF02345; Tr; SM00181; Tr; SM00274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00137; MAM;
SM00214; VWC;
SM00216; VWD;
                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IPR000561;
; IPR003645;
; IPR000998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPRO03328;
IPRO01007;
IPRO01846;
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     2460
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1670
2057
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     MAM_domain.
TIL_Cysrich.
TILa_Cysrich.
VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VWF_D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Folu
                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; EGF-like domain; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1.
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      VWFD
VWFD
VWFD
                                                                                                                                                                                                                                                                                                                 ZONADHESIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                  80 X HEPTAPEPTIDE REPEATS (MUCIN-LIKE DOMAIN).
                                                                                                                      10
6 (PARTIAL).
7 (PARTIAL).
8 (PARTIAL).
9 (PARTIAL).
10 (PARTIAL).
2 (PARTIAL).
2 (PARTIAL).
3 (PARTIAL).
4 (PARTIAL).
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5 (PARTIAL).
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1 (PARTIAL).
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15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member activator and CAML interactor).
TRIPRESTIB OR TACI.
HOmo sapiens (Human),
Eukheria; Primates; Catarrhini; Hominida
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                                                                 MEDLINE=97458245; PubMed=9311921; von Buelow G.-U., Bram R.J.; "NF-AT activation induced by a CA
                                                                                                                                              SEQUENCE FROM
TISSUE-B-cell;
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RX MEDLINE-21170294; PubMed=10973284;

RA YU G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,

RA WCGAbe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,

RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,

RA MCCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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PROSITE; PS00652; TNFR_NGFR_1; 1.

PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.

Receptor; Immune response; Signal-anchor;
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CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA 40

Matches Query Match Best Local (

Similarity

28.2%;

Conservative

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Mismatches

Pred.

% 67.5; No. 0.

DB 1; 15;

Length Indels

293;

1;

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RESULT 7
T13C_MOUSE
ID C_MOUSE
ID C_MOUSE
OG Q9DBDD
DT 15-JUN
DT 15-JUN
DT 15-JUN
DT TION
DE activa
DE activa
DE ACTIVA
DO CEUKARY
OC EUKARY
OC MARMALI
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RA THOMPS
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RP SEQUEN
RA CANCIC
RN [3]
RP SEQUEN
RA AIZEN
RA AIZEN
RA AIZEN
RA AIZEN
RA BICOMN
RA GUSTI
RA BICON
RA GUSTI
RA WYOSH
RA WYOSH
RA WYOSH
RA WYOSH
RA WYOSH
RA HAILE
RA HAILE
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                                                                                                                                                                 RA Arakawa T. Hara A. Fukunishi Y. Konno H. Adachi J. Fukuda S. Ra Aizawa K. Izawa M. Nishi K. Kiyosawa H. Kondo S. Yamanaka I. Ra Saito T. Okazaki Y. Gojobori T. Bono H. Kasukawa T. Saito R. Ra Saito T. Okazaki Y. Gojobori T. Bono H. Kasukawa T. Saito R. Ra Fleischmann W. Gaasterland T. Gissi C. King B. Kochiwa H. Ra Kuchi P. Lewis S. Matsuo Y. Nikaido I. Pesole G. Quackenbush J. Ra Kuehi P. Lewis S. Matsuo Y. Nikaido I. Pesole G. Quackenbush J. Ra Kuchi P. Lewis S. Matsuo Y. Nikaido I. Pesole G. Quackenbush J. Ra Schriml L.M. Staubli F. Suzuki R. Tomita M. Wagner L. Washio T. Ra Sakai K. Okido T. Furuno M. Aono H. Baldarelli R. Barsh G. Ra Blake J. Boffelli D. Bojunga N. Carninci P. de Bonaldo M.F. Ra Blake J. Boffelli D. Bojunga N. Carninci P. de Bonaldo M.F. Ra Gustincich S. Hill D. Hofmann M. Hume D.A. Kaniya M. Lee N.H. Ra Lyons P. Marchionni L. Mashima J. Mazzarelli J. Mombaerts P. Ra Oustincich S. Ringwald M. Rodriguez I. Sakamoto N. Ra Nordone P. Ring B. Ringwald M. Seya T. Shibata Y. Storch K.-F. Ra Sasaki H. Sato K. Schoenbach C. Seya T. Shibata Y. Storch K.-F. Ra Suzuki H. Toyo-oka K. Wang K.H. Weitz C. Whittaker C. Wilning L. Ra Nordone P. Ring H. Yoshida K. Hassegawa Y. Kawaji H. Kohtsuki S., Ra Wynshaw-Boris A. Yoshida K. Hassegawa Y. Kawaji H. Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21442025; PubMed-11509692;
Thompson J.S., Bixler S.A., Qian F., Vora K., S
Cachero T.G., Hessian C., Schneider P., Sizing
Strauch K., Zafari M., Benjamin C.D., Tschopp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1:
STRAIN-C57BL/6J; TISSUE-Small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yan M., Brady J.R., Chan B., Lee W.P. Cancro M.P., Grewal I.S., Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). STRAIN-BALB/C: TISSUE-B-cell lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activating factor receptor) (
3) (B-cell maturation defect)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is mutated in a mouse strain with severe B Curr. Biol. 11:1547-1552(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 293:2108-2111(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFRSF13C OR BAFFR OR BCMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9D8D0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T13C_MOUSE
  Harless S.M.,
Hilbert D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a novel receptor for B lymphocyte stimulator is mutated in a mouse strain with severe B cell deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21475520; PubMed=11591325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "BAFF-R, a newly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ambrose C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                            MEDLINE * 21614654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J., Shinagawa A., Shibata K.,
                                                                                                           lonal annotation of 409:685-690(2001).
  Lentz V.M.,
Hayes C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identified TNF
                                               PubMed-11747827;
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Rodentia;
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    Sah A.P., Hs
Cancro M.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAFF receptor) (BAFF-R) (BLyS receptor
                                                                                                                               full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee W.P., Hsu B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intestine
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                      Hsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                      B.L.,
                                                                                                                                  mouse
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g I.D., Mullen C.,
J., Browning J.L.,
                                                                                                                                  CDNA
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                        Clise-Dwyer
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                                                                                                                                  collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishii Y.,
Fukuda S.,
manaka I.,
Saito R.,
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TISSUE-Brain;
MEDLINE-97301565; PubMed-9157966;

SEQUENCE FROM N.A. NCBI_TaxID-9031; Archosauria; Eukaryota; Metazoa;

Aves; Neognathae;

Chordata; Craniata; Vertebrata;

Galliformes; Phasianidae; Phasianinae;

Euteleostomi;

Morwald S., Yamazaki H., Bujo H., Kusunoki J., K Morisaki N., Nimpf J., Schneider W.J., Saito Y.; "A novel mosaic protein containing LDL receptor

Kanaki T.,

Seimiya K.,

elements is highly

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RESULT
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Best Local
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                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sortilin-related receptor (Sorting protein-related receptor containing LDLR class A repeats) (SorLA) (SorLA-1) (Low-density lipoprotein receptor relative with 11 ligand-binding repeats) (LDLR relative with 11 ligand-binding repeats) (LDLR relative with 11 ligand-binding sepaces) (LR11) (Fragment).
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLys. Promotes the survival of mature B-cells and the B-cell response.
-i- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
-i- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peripheral B lymphocyte numbers.
Curr. Biol. 11:1986-1989(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q98930;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SORL_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1919299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Competition for BLyS-mediated signaling through Bcmd/BR3 regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 QCSQNEYFDSLLHACIPCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Highly expressed in spleen and testis; detected at lower levels in lung and thymus.

DISEASE: Defects in TNFRSF13C are a cause of severe B-cell deficiency. B-cell deficient strain A/MySnJ has a 4.7 kb insert in the BAFFR gene leading to an altered C-terminus. The mutant is not detectable. B-cell lymphopolesis is normal, but the life span of peripheral B-cells is much reduced.

SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         produced by alternative splicing.
TISSUE SPECIFICITY: Highly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCNQTECFDPLVRNCVSCEL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF373847;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amune .
e splicing.
71
92
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21
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133
175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175
38
35
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38
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143
18798
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BAB25490.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.4%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL SIGNAL-ANCHOR (TYPE III (POTENTIAL). (POTENTIAL). CYTOPLASHIC (POTENTIAL). TNFR-CYS (PARTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; DB 1
Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
N-LINED (GLONAC...) (POTENTIAL).
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28BC7C1A02FB87EF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kb insertion
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AT conserved in humans and chickens.";

A Arterioscler. Thromb. Vasc. Biol. 1:996-1002(1997).

A Arterioscler. Thromb. Vasc. Biol. 1:996-1002(1997).

C -1- FUNCTION. LIKELY TO BE A MULTIFUNCTIONAL ENDOCYTIC RECEPTOR, THAT MAY BE IMPLICATED IN THE UPTAKE OF LIFOPROTEINS AND OF PROTEASES.

BINDS LDL, THE MAJOR CHOLESTEROL-CREATEN OF PLASMA,

C AND TRANSPORTS IT INTO CELLS WE PLADOCYTOSIS. BINDS THE RECEPTOR-CASSOCIATED PROTEIN (RAP). COULD PLAY A ROLE IN CELL-CELL

ASSOCIATED PROTEIN (RAP). COULD PLAY A ROLE IN CELL-CELL

C INTERACTION. BOTH ESTROGEN STATUS AND CHOLESTEROL LEVELS LACK

REGULATORY EFFECTS ON THIS RECEPTOR.

C -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

TISSUE SPECIFICITY: EXPRESSED ABBNDANTLY IN BRAIN. PRESENT IN THE

TESTES, ADREMAL GLANDS AND DETECTABLE IN THE LUNG.

C -1- SIMILARITY: CONTAINS 5 BNR REPEATS.

C -1- SIMILARITY: CONTAINS 1 LOL-RECEPTOR CLASS A DOMAINS.

-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y08109; CAA69324.1; -.
HSSP; P01130; 1AJJ.
InterPro; IPR000561; EGF-like.
InterPro; IPR003961; FN_III.
InterPro; IPR002860; GH_BNR.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR0000172; LdL_receptor_rep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00041; fn3; 1
Pfam; PF00057; ldl_rc
Pfam; PF00058; ldl_rc
Pfam; PF02012; BNR; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; Pr00057; ldL_recept_a; 11.
Pfam; Pr00059; ldL_recept_b; 5.
Pfam; Pr02012; BNR; 5.
Pfam; Pr02012; BNR; 5.
Pfam; Pr02012; BNR; 5.
PRNTS; PR00261; LDLRECEPTOR.
SWART; SW001019; LDLa; 11.
SWART; SW00102; LDLa; 11.
SWART; SW00102; LDLa; 11.
SWART; SW00135; LY; 5.
PROSITE; PS01108; EGF; 1.
PROSITE; PS01209; LDLRA_1; 11.
PROSITE; PS01209; LDLRA_1; 11.
PROSITE; PS01209; LDLRA_2; 11.
Endocytos1s; Receptor; EGF-like domain; Repeat; Glycoprotein; LDL;
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P98167;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seque
16-OCT-2001 (Rel. 40, Last annot
SCO-spondin (Fragment).
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TISSUE-*Ependymocyte;
MEDLINE-*9638614; pubMed-*8743952;
Gobron S., Monnerie H., Meiniel R., Creveaux I., Lehmann W.,
Lamalle D., Dastugue B., Meiniel A.;
*SCO-spondin: a new member of the thrombospondin family secreted
the subcommissural organ is a candidate in the modulation of neur
  aggregation.";
J. Cell Sci. 109:1053-1061(1996).
-i- FUNCTION: INVOLVED IN THE MODULATION
-i- SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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actyla; Ruminantia; Pecora; Bovoidea
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- DEVELOPMENTAL STAGE:
- SIMILARITY: BELONGS TO
- SIMILARITY: CONTAINS:
- SIMILARITY: CONTAINS:
- SIMILARITY: CONTAINS:

TISSUE

SPECIFICITY:

SUBCOMMISSURAL ORGAN

EMBRYO

SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-I DOMAINS.
SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.

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(See http://www.isb-sib.ch/announce/

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PROSITE; PS01285; FA58C_1; 1
PROSITE; PS01296; FA58C_2; 1
PROSITE; PS01209; LDLRA_1; 3
PROSITE; PS50068; LDLRA_2; 3
PROSITE; PS50092; TSP1; 4
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; PF00093; vwc; 1.
;; PF00754; PS_F8_type_C
;; PF01026; TIL; 1.
; SM00231; FA58C; 1.
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LDL-RECEPTOR CLASS
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F5/8 TYPE C.
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15-JUN-2002
15-JUN-2002
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MEDLINE=97480720; pubMed=933955;
Hadjantonakis A.-K., Sheward W.J., Harmar
Hoovers J.M.N., Little P.F.R.;
"Celsr1, a neural-specific gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mech. Dev. 112
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Mammalia; Eutheria;
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                                                                                                   kidney and epithelia.

TISSUE SPECIFICITY: Expressed in the brain, where it is localized principally in the ependymal cell layer, choroid plexus and the area postrema. Also found in spinal chord and in the eye.

SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.

SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                          Signaling during nervous system formation.
SUBCELULIAR LOCATION: Integral membrane protein.
DEVELOPMENTAL STAGE: First detected at E6. Predominantly expresse in the developing CNS, the emerging dorsal root ganglia and cranial ganglia. In the CNS, expression is uniform along the rostrocaudal axis. During gastrulation, it is expressed in the vicinity of the primitive streak, and becomes present in that area at late gastrulation. At E10, detected in ventricular zones (VZ), but not in marginal zones (MZ), and weakly in other structures. Between E12 and E15, a high expression is present in
                                                                                                                                                                                                                                                                                                                         the VZ in all brain areas. No expression in differenciated neuronal fields. In the newborn and postnatal stages, expression
                                                                                                                                                                                                                                                                                                       remains restricted to the
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45:97-104(1997).
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Rodentia;
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s Institute. The
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Sciurognathi; Muridae;
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HSSP; P00749; 1URK.

InterPro; IPR000152; Asx_hydro
InterPro; IPR0002126; Cadherin.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000832; GPCR secr
InterPro; IPR0002049; Laminin_E
InterPro; IPR0010791; Laminin_E
InterPro; IPR0010791; Laminin_E
InterPro; IPR0010791; Laminin_E
InterPro; IPR00108; EGF; 1.
Pfam; PF00008; EGF; 5.
Pfam; PF00008; EGF; 1.
Pfam; PF000053; Laminin_EGF; 1.
Pfam; PF000053; Laminin_G; 1.
PFAM; PF000053; Laminin_G; 1.
PFAM; PF00054; Laminin_G; 1.
PFAM; PF00054; Laminin_G; 1.
SMART; SM00101; EGF_11ke; 6.
SMART; SM00101; EGF_11ke; 6.
SMART; SM00100; EGF_11ke; 6.
SMART; SM00100; EGF_11ke; 6.
SMART; SM00100; EGF_11ke; 6.
SMART; SM002032; CADHERIN_1;
PROSITE; PS00232; CADHERIN_1;
PROSITE; PS00232; CADHERIN_1;
PROSITE; PS00232; CADHERIN_1;
PROSITE; PS00232; CADHERIN_2;
PROSITE; PS00232; CADHERIN_1;
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PROSITE; PS00232; CADHERIN_1;
PROSITE; PS00232; G_PROTEIN_RE
PROSITE; PS00650; G_PROTEIN_RE
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; SM00018; EGF_LAM; 1.
; SM00001; EGF_LAM; 1.
; SM000008; HOTMR; 1.
; SM00008; HOTMR; 1.
; SM00282; LAMG; 2.
TE; PS00010; ASX_HYDROXYL; 2.
TE; PS00010; ASX_HYDROXYL; 2.
TE; PS00023; CADHERIN_1; 7.
TE; PS00128; EGF_1; 6.
TE; PS00128; GFCT; 2.
TE; PS00129; GFCTEIN_RECEP_F2_1; FALSE_NEG.
TE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
TE; PS00650; G_PROTEIN_RECEP_F2_4; 1.
TE; PS0027; LAMININ_TYPE_EGF; 1.
TE; PS0027; LAMININ_TYPE_EGF; 1.
TE; PS0028; LAM_G_DOMAIN; 2.
TE; PS0025; LAM_G_DOMAIN; 2.
TE; PS01248; LAMININ_TYPE_EGF; 1.
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EGFLAMININ.
GPCRSECRETIN.
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        Celsr1
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Cadherin.
EGF-like.
GPCR_secretin.
hormn_receptor.
Laminin_EGF.
Laminin_G.
PKD_cys_rich.
POTENTIAL.

CADHERIN EGF LAG SEVEN-PAR
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CYTOPLASMIC (POTENTIAL).

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EGF-LIKE 2, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
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LAMININ G-LIKE 1.

EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
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EGF-LIKE 1, CALCIUM-BINDIN
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15-JUL-1999 (Rel. :
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SEQUENCE 63 AA;
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15-JUL-1999 (Rel. 38, Last annotation update)
Chymotrypsin/elastase isolnhibitor 1 (C/E-1 inhibitor).
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
MEDLINE-92381036; PubMed-1512259;
Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U., Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
"Cloning and functional expression of Dfurin2, a subtilisin-like proprotein processing enzyme of Drosophila melanogaster with mult repeats of a cysteine motif.";
J. Biol. Chem. 267:17208-17215(1992).
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Structure 2:679-689(1994).

-i- FUNCTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES

-i- FUNCTION: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.
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                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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01-APR-1993 (Rel.
15-JUL-1998 (Rel.
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InterPro; IPR000561; EGF-like.
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InterPro; IPR002174; Furin-like.
InterPro; IPR002084; P_domain.
InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9ULTO;
                                                                                                                                                                                                                                                                                                                                                                              REPEAT
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Res. 6:329-336(1999)
                                                                                       ARATH
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RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P., Ra Langham S.-A., McCullagh B., Bilham L., Robben J., Rangham S.-A., McCullagh B., Bilham L., Robben J., Rangham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., Rangham S.-A., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Rangherger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Ra Heitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Rangham S., Van Staveren M., Dirkse W., Rangham S., Van Staveren M., Dirkse W., Rangham P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Rangham P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Rangham P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Rangham M., Lamberth S., Van den Daele H., Rangham M., Landberth S., Van den Daele H., Rangham M., Landberth S., Van den Daele H., Rangham M., Rangham M., Quaill M., Bray-Allen S., Rangham M., Maarse A.C., Schaefer M., McLay K., Mayes R., Rangham M., Marse A.C., Schaefer M., McLay K., Mayes R., Rangham D., Vitale D., Liguori R., Piravandi E., Rangham M., Marse A.C., Schaefer M., Mueller Auer S., Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Rangham M., Vandenbol M., Bargues M., Terol D., Jesse R., Rangham M., Vandenbol M., Bargues M., Terol D., Jesse T., Rangham D., Haase D., Llemcke K., Mewes H.-W., Stocker S., Prancs P., Bielke C., Rangham M., Marsey J., Shett P., Cordes M., Abboths A., Stocker S., Parnelle B., Bent E., Johnson S., Terol D., Jesse T., Rangham M., Marray J., Shett P., Cordes M., Abboth A., Soctt K., Johnson D., Rangham M., Marray J., Shet P., Cordes M., Abboth A., Schiller L., Rangham D., Berghoff A., Jones K., Done K., Cotton M., Joshu C., Rangham S., Marra M., Martienssen R., McCombie W.R., Shah R., Sh
                                                                                                                                                    -!- FUNCTION: INVOLVED IN LATE STAGES OF SEED M
STEPS OF GERMINATION.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: SILIQUES AND DRY SEEDS.
-!- PTM: SIX DISULFIDE BONDS MAY BE PRESENT.
-!- SIMILARITY: BELONGS TO THE GAST1 FAMILY.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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MEDLINE-95244835;
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Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgartner M., de Simone V., Obermaler B., Mache R., Mueller M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402:769-777(1999)
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ed to the tomato GAST1 gene.";
Mol. Biol. 27:743-752(1995).
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Matches 15
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Q28983;
Q1-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
NCBI_TaxID-9823;
[1]
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J. Biol. Chem. 270:26025-26028(1995).
-I- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO TH
-I- FUNCTION: BINDS IN A SPECIES SPECIFIC MANNER TO TH
-I- OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION
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                                                                                          -I- SUBGULT: PROBABLY PORMS COVALENT OLIGOMERS.
-I- SUBGULTUAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
-I- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS. NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDLDYMIS.
-I- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.
-I- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
-I- DOMAIN: THE VWFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
-I- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX. PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890; 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 1658-1667; 1777-1795 AND 1914-1221.
STRAIN-Meishan; TISSUE-Testis;
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                                                                                                                                                                                                                                                                                                                                                                                     "A sperm membrane protein that binds in a sthe egg extracellular matrix is homologous
                                                                                                                                                                                                                                                                                                                                                                                                                 Hardy D.M., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96064658; PubMed=7592795;
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                                        CAPACITATION.
- SIMILARITY: CONTAINS 2
- SIMILARITY: CONTAINS 4
- SIMILARITY: CONTAINS 1
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15; Conserver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor.
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is copyright. It is produced through stitute of Bioinformatics and the EM
                                        2 MAM DOMAINS.
4.5 VWFD DOMAINS
1 EGF-LIKE DOMAIN
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Pfam; PF00629; MAM; 2.
Pfam; PF01826; TIL; 5.
Pfam; PF02345; TILa; 5.
SMART; SM00181; EGF; 1.
SMART; SM00137; MAM; 1.
SMART; SM00214; VWC; 2.
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InterPro; IPR003328; TILa_Cysrich.
InterPro; IPR001007; VWF_C.
InterPro; IPR001846; VWF_D.
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InterPro; IPR000998; MAM_domain.
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Q26489 spodoptera
O9vw81 drosophila
O8vx88 drosophila
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Q9y6r7 homo sapien	Q9Y6R7	4	2843		55.5	ω
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Q94lu6 oryza sativ	Q94LU6	10	881		55.5	Ë
Q94lu3 oryza sativ	Q94LU3	10	675		55.5	5
Q9ve40 drosophila	Q9VE40	ഗ	225		55.5	39
Q9ep23 hepatitis c	Q9EP23		146		55.5	8
P90891 caenorhabdi	P90891		2972		56	37
Q8rz84 oryza sativ	Q8RZ84		260		56	8
Q9vlt6 drosophila	Q9VLT6		2820		56.5	ŭ
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Q9ep28 hepatitis c	Q9EP28	12	146		56.5	ũ
	Q9VB21	S	1511		57	ະ
Q96dn2 homo sapien	Q96DN2	4	955		57	Ξ
Q18761 caenorhabdi	Q18761	S	838		57	õ
Q27422 caenorhabdi	Q27422	ഗ	838		57	9
Q9c091 homo sapien	090091	4	752		57	8
Q9s9j8 arabidopsis	8r6S60	10	653		57	27
017692 caenorhabdi	017692	S	502		57	6
7	Q9BUS3	4	450		57	5
	Q9PVD4	13	387		57	4
0	OMAMO	10	321		57	ພ
	Q24301		1679		57.5	2
	08SZS2		1376		57.5	1
017970 caenorhabdi	017970		1513		58	ö
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O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-NOV-1998 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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NON_TER 499 499
SEQUENCE 499 AA; 5419(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of interactions between trefoil peptides and members of the mucin protein family using the yeast two-hybrid system."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ010752; CAA09343.1; -.
HSSP; P56682; ICCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-STOMACH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
InterPro; IPR002919; TIL_Cysrich.
InterPro; IPR001846; VWF_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
                                                                       5 CSQNEYFDSLLHACIPCQLRCSSNTPPLT 33
                                                                                                                                                                                          Similarity
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                         54190 MW;
                                                                                                                                                                                      30.3%;
                                                                                                                                              Score 72.5; DB 11; Length Pred. No. 0.013; Indels 1; Mismatches 7; Indels
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Q9BIO7
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Best Local
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Pfam; PF01826; TIL; 25.
Pfam; PF001845; TILa; 25.
Pfam; PF00094; vwd; 4.
SMART; SM00001; EGP_1ike; 1.
SMART; SM00174; FOLN; 21.
SMART; SM00137; VWC; 25.
SMART; SM00214; VWC; 25.
SMART; SM00216; VWD; 4.
Q9BIO7;
Q9BIO7;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                            PROSITE;
PROSITE;
PROSITE;
EGF-like
                                                                                                                                                                        3297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21138439; PubMed=11239002; Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Wilson M.D., Riemer C., Schwartz S., Scherer S.W., T. Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., T. Miller W., Koop B.F.; Gene-dense ACHE/TFR2 regromosome 7922 with the orthologous region on mouse chromosome 7922 with the orthologous region on mouse nucleic Acids Res. 29:1352-1365(2001).
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Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheung T.L., Wilson M.D., "Genomic Basis of Inter- & Domain Structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-129/SV;
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                                                                                                                                                                                                           4 QCSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC 38
                                                                                                                                                                      QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o; IPR000998; MAM_domain.
o; IPR003328; TILA_CYSTich.
o; IPR003919; TILCCYSTich.
o; IPR001007; VWF_C.
o; IPR001846; VWF_D.
                                                                                                                                                                                                                                                                                                                                       domain; Gl;
5374 AA;
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PS01186; EGF_2; 18.
PS50060; MAM_2; 3.
  (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                         Conservative
                                                                PRELIMINARY;
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AA; 579536 MW;
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Pred. No. 0.37
5; Mismatches
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Variation
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Tsui L.-C.,
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Best Local (
                                          InterPro; IPR00257; Chitin_bind_perA.
InterPro; IPR002794; Ketoacy1-synt.
InterPro; IPR003571; Snake_toxin.
InterPro; IPR003571; Snake_toxin.
InterPro; IPR002899; WR1/EB.
Pfam; PF01607; CBM_14; 2.
SMART; SM00289; WR1; 12.
                                                                                                                                                                                                             Geisel C.;
"The sequence of C. e
Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q22378
Q22378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Willhoeft U., Campos-Gongora E., T
"Introns of Entamoeba histolytica
protist 152:149-156(2001).
EMBL; AJ409106; CAC34072.1; -.
Interpro; IPR002174; Furin-like.
SMART: SM00261; FU; 7.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; PROSITE; PS0072; SNAKE_TOXIN; UNKNOWN. Hypothetical protein. SEQUENCE 966 AA; 102460 MW; B565A30
                                                                                                                   "Direct Submission.";
Submitted (JUL-2001) to the EMBL; U39644; AAA80360.2; -. HSSP; P10969; lWGT.
                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Waterston R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002174; FU
SMART; SM00261; FU; 7.
NON_TER 718 718
SEQUENCE 718 AA; 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Putative cysteine surface protein (Fragment).
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium. Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                                                                                                                          None
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12; Conserv
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BLrel. 21, Last:
5 kDa protein.
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inae; Caenorhabditis.
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EMBL/GenBank/DDBJ
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Pred. No. 0.09
6; Mismatches
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 B565A3CDD25216D9 CRC64;
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RA Johannson S., Birk R., Hakiy N., Franke P., Kodelja V., Kannicht C., Orfanos C.E., Johannson S., Goerdt S.;
RT "Stabilin-1 and stabilin-2 constitute a novel family of fasciclin domain-containing adhesion molecules associated with endothelial-
RT macrophage differentiation and angiogenic processes.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

SR EMBL; AJ295695; CACE2105.1;

R InterPro; IPR000538; BIgH3_fasciclin.

IR InterPro; IPR000538; EGF-like.

R InterPro; IPR000539; Laminin_EGF.

R Pfam; PF00008: RGF- 2n
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Matches 13
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Best Local :
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Pfam; PF002469; Fasciclin; 5.

Pfam; PF00193; Xlink; 1.

ProDom; PD000918; Link; 1.

SMART; SM00181; EGF; 24.

SMART; SM00445; LINK; 1.

SMART; SM00445; LINK; 1.

PROSITE; PS001022; EGF_1; UNKNOWN_7.

PROSITE; PS01186; EGF_2; UNKNOWN_16.

PROSITE; PS011248; LAMININ_TYPE_EGF; UNISEQUENCE 2551 AA; 276992 MW; 60A44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                            Q8R4W8;
Q8R4W8;
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                                                                                                         01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
  SEQUENCE FROM N.A. Mizuno K., Irie S., "Identification of
                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                  TRAF3 binding protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                               l Similarity
15; Conserv
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13; Conser
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, Sato T.-A.;
novel TRAF3 binding protein, T3BP, which increases
                                                            Chordata;
Rodentia;
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30.0%;
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Pred. No. 0.24
7; Mismatches
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Pred. No. 0.86
4; Mismatches
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                                                            Craniata; Vertebrata;
Sciurognathi; Muridae;
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60A44651CCC2BE69 CRC64;
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                                                                                                                                                                                                                                                                                     Length 2551;
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                                                                                                                                                                                                                                                               Indels
                                                            Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                               22;
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Matsuda H.A., Ashburner M., Battalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Battalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Heischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Wyoshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wyoshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                  Matches
                                                                                Query Match
Best Local :
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01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-C57BL/6J; TISSUE-IN VITRO FERTILIZED EGGS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9D351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellular F-actin content.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF350257; AAL83914.1; -.
SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;
                                                                                                                                PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFFC CRC64;
                                                                                                                                                                                                 ProDom; PD000003; Znf_C2H2; 1. SMART; SM00355; ZnF_C2H2; 3.
                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AKO18361; BAB31177.1; -.
HSSP; P08047; 1SP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                  MGD; MGI:1923003; 7420700M05Rik.
InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                    Pfam; PF00096; zf-C2H2;
                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                               4 QCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
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RCNEREWESQLIRSLPEHGVRCPSQLAPIPFQNYCQRSI
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10; Conserv
                                                                                  Similarity
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Metazoa; Chordata; C

Metazoa; Rodentia; S
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                                                                                26.4%;
28.2%;
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Last sequence update)
Last annotation update)
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Pred. No.
                                                               9
                                                                                Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                 Mismatches
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1.25;
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                                                                                               Length 341;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukuda S., amanaka I., Saito R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; A;
Pterygota; Neoptera; I
Ephydroldea; Drosophi
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9VW81;
01-MAY-2000
01-MAY-2000
01-JUN-2002
CG7348 prote
CG7348
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01-NOV-1996
01-JUN-2002
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Q26489;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S. Alburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Beallew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1150
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Spodoptera frugiperda (Fall armyworm).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Pterygota; Neoptuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00261; FU, 10.

PROSITE; PS00136; SUBTILASE_HIS;
PROSITE; PS00137; SUBTILASE_HIS;
PROSITE; PS00138; SUBTILASE_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00723; SUBTILISIN ProDom; PD000717; P_domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and functional characterization of FURIN from Spodoptera frugiperda (Sf9) cells.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-SF9;
Cleplik M., Klenk H.;
                                                                                                                                                                                                                                                                                                                                    MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VW81
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Q99405; 1MPT.
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endopterygota; Dip
ilidae; Drosophila.
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37.5%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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annotation update)
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..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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RA Glodek A. Goog F. Gorrell J.H. Gu Z. Gubar P. Harris M.,

RA Harris N.L. Harvey D., Heiman T.J., Wei M.-H. Ibeqwam C.,

RA Harris N.L. Howston K.A. Howland T.J. Wei M.-H. Ibeqwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA McIvilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K., Saunders R.D.C., Scheeler F., Shen H.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Welnstock G.M., Welssenbach J.,

RA Wang Z.-Y., Wassarman D.A., Welnstock G.M., Welssenbach J.,

RA Yelliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Yell X.H., Zhong F.N., Zhong W., Zhong G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;

RT Telegenome sequence of Drosophila melanogaster.*;
   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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01-JUN-2002
01-JUN-2002
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Cherry J.M., C
de Pablos B., I
                                                                                                                    STRAIN-BERKELBY;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,

Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,

Miranda A., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                           Drosophila
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8SZ58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dave de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dodgson K., Doup L.E., Downes M., Dugan-Rocha S., Dunko Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of Drosophila Science 287:2185-2195(2000).
                                                         SEQUENCE
                                                                          Submitted (DEC-2001) to the EMBL; AY071103; AAL48725.1;
                                                                                                               Celniker S.;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Ephydroidea;
                                                                                                                                                                                                                                                                                                          Pterygota;
                                                                                                                                                                                                                                                                                                                                                                 CG7348
                                                                                                                                                                                                                                                                                                                                                                             RE16222p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0036940; CG7348.
InterPro; IPR002557; Chitin_bind_PerA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCSVGNYFDPARRACLPVAISAAHQCSCVLPDNATLANPSDCETY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF01607; CBM_14; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE003514; AAF49068.1; -.
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J.M., Cawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00494; ChtBD2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                       Neoptera; Endopterygota; Diptera;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                           melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                         353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                         Α,
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31.1%;
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21,
21,
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                                                         ₩;
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Last sequence update)
Last annotation update)
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                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 60.5; In Pred. No. 0.61
5; Mismatches
     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1C66916504FD130B CRC64;
                                                         F5AB27B9A6FF9921 CRC64;
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     60.5;
No. 0.
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DB
.61;
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Dew I., Diet
                                                                                                                                                                                                                                                                                                              Brachycera; Muscomorpha;
                      Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dietz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.M.,
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Similarity

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RESULT 12
Q9GQ45
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBSPM4 PRELIMINARY;
OBSPM4;
O1-JUN-2002 (TrEMBLrel. 2:
O1-JUN-2002 (TrEMBLrel. 2:
O1-JUN-2002 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                Q9GQ45 PRELIMINARY; PRT; 54
Q9GQ45;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequen
Q1-JUN-2002 (TrEMBLrel. 21, Last annota
                     InterPro;
InterPro;
                                                        InterPro;
InterPro;
                                                                                       Mansouri M., Ey P.L.;

"A segment of a vsp72-like gene homolog from a Giardia intestinalis isolate.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ EMBL; AF298862; AAG37862.1;

HSSP; P00136; 2CT3.
                                                                                                                                                                                                                                               Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae;
NCBI_TaxID-5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glia 32:177-191(2000).
EMBL; AJ416457; CAC94914.1; -.
SEQUENCE 5146 AA; 543576 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCO-spondin.
SCO-SPONDIN.
                                                                                                                                                                                            STRAIN-AD-1;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=SUBCOMMISSURAL ORGAN; MEDLINE=20465125; PubMed+11008217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meiniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-SUBCOMMISSURAL ORGAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1814 VFHACVPCPLTCDDISGQATC 1834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outgrowth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCO-spondin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gobron S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Subcommissural organ/Reissner's SCO-spondin, a glycoprotein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 LLHACIPCQLRCSSNTPPLTC : |||:||:||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QCSQNEYFDSLLHACIPCQL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
9; Conserv
IPR000564; 2Fe2S_ferredoxin.
IPR000345; CytC_heme_bind.
IPR000561; EGF-like.
IPR002174; Furin-like.
IPR002350; kazal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                         548
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                                                                                                                             databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5146;
                                                                                                                                                          type A-I
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Best Local S
Matches 15
                                                SMART; SM00112; CA; 9.
SMART; SM00180; EGF_Lam; 1.
SMART; SM00001; EGF_1ike; 6.
SMART; SM00003; GPS; 1.
SMART; SM00008; HormR; 1.
SMART; SM000282; LamG; 2.
                                                                                                                                                                                                                                      Pfam; PF00002; 7tm_2; 1.
Pfam; PF0002B; cadherin; 9.
Pfam; PF0000B; EGF; 6.
Pfam; PF01825; GPS; 1.
Pfam; PF02793; HRW; 1.
EGF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
NON_TER
SEQUENCE
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035161;
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
 PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                           Pfam; PF00053;
Pfam; PF00054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 45:97-104(1997).
-i- SIMILARITY: CONTAINS 9
-EMBL; AF031572; AAC68836.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Celsr1, a neural-specific gene
transmembrane receptor, maps to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97480720; PubMed-9339365;
Hadjantonakis A.K., Sheward W.J.,
Hoovers J.M., Little P.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57/BL6; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELSR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seven-pass transmembrane receptor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002049;
InterPro; IPR001791;
InterPro; IPR000203;
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR002126; Cadherin.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 22qter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000832; GPCR_secretin.
InterPro; IPR001879; hormn_receptor.
InterPro; IPR002049; Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1100883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGOCSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00181; EGF; 2.
SM00001; EGF_like;
SM00261; FU; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.9%;
l Similarity 36.6%;
l5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00197; 2FE2S_FERREDOXIN; UNKNOW PS00190; CYTOCHROME_C; UNKNOWN_1. PS00282; KAZAL; UNKNOWN_1.
                                    PS00010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                548 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                              l; EGFLAMININ
                                                                                                                                                                                            laminin_G;
5; CADHERIN.
                                                                                                                                                                                                                             laminin_EGF; 1.
 : ASX_HYDROXYL; (CADHERIN_1; 6.; CADHERIN_2; 9.
                                                                                                                                                            GPCRSECRETIN
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                                                                                                                                                                                                                                                                                                                                  PKD_cys_rich.
                                                                                                                                                                                                                                                                                                                                                   Laminin_G.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 59.5; D
Pred. No. 1.3;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578FE4FDA0A2CF0E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse chr
                                      UNKNOWN_2.
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Best Local S
Matches 15
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Best Local
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O18118
O18118
O1-JAN 1998 (TrEMBLrel. 0
01-JAN 1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
T23F1.6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O77419 PRELIMINARY; cn., O77419; O77419; O77419; O1-NOV-1998 (TrEMBLrel. 08, Created) O1-NOV-1998 (TrEMBLrel. 08, Last sequence update) O1-NOV-1998 (TrEMBLrel. 21, Last annotation update) Chymotrypain/elastase inhibitor-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
SEQUENCE
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SIGNAL
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PROSITE; P$01186; EGF_2; 2.

PROSITE; P$50217; G_PROTEIN_RECEP_F2_3; 1.

PROSITE; P$50261; G_PROTEIN_RECEP_F2_4; 1.

PROSITE; P$01248; LAMININ_TYPE_EGF; UNKNOWN_1.

Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein;
Receptor; Signal; Transmembrane.
                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98297373; PubMed-9635450;
Lu C.C., Nguyen T., Morris S., Hill D., Sak
"Anisakis simplex: mutational bursts in the
serine protease inhibitors from an ascarid
Exp. Parasitol. 89:257-261(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001
 SEQUENCE FROM Wilkinson J.;
                                                                                                                                                                                                                                                                                                                                                            EMBL; U94499; AAC61300.1; -. HSSP; P07851; 1EAI. InterPro; IPR002919; TIL_Cysrich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ascaris suum (Pig roundworm)
Eukaryota; Metazoa; Nematoda
Ascarididae; Ascaris,
                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01826; TIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6253;
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                                                                                                                                                                                                                                       QCSQNEYFDSLLHACIPCQLRCS--SNTP-PLTCQR-YCNAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQ-----RYCN
                                                                                                                                                                                                                 RCGPNEVWTE----CTGCEMKCGDPENTPCPLMCRRPSCECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                 15; Conserv
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14; Conservative
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27 30
3034 AA;
                                                                                                                                                                                                                                                                                                                62 AA;
                                                                                                                                                                                                                                                                 Conservative
                                                Peloderinae;
                                                                                                                                                                                                                                                                                                                            62
             Z.A
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A; 330477
                                                                                                                                                                                                                                                                                                              62
6794 MW;
                                               Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematoda;
                                                                                                                                                                                                                                                                           24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.9%;
                                                                                                        05,
19,
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Last sequences
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SEVEN-PASS TRANSMEMBRANE RECEPTOR
MW; EFF38180AF5ED8A8 CRC64;
                                                                                                                                                                                                                                                                           Score 59; DB 5
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Ascaris lumbricoides).
Chromadorea; Ascaridida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                               154CE25A375E0B2C CRC64;
                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                        sequence update)
annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                        reactive site of nematode.";
                                                           Rhabditida;
                                                                                                                                                                                                                                                                                        5; Length 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                           Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                       centers
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Matches 13
                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81129; CAB03405.1; -.
InterPro; IPR003341; DUE139.
Pfam; PF02363; DUF139; 7.
SEQUENCE 330 AA; 36605 MW;
                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-99069613;
                                                                                                                                                                   none;
                                                                                                                                                                                                              Submitted (OCT-1996)
                                                                                                                                                       "Genome sequence of the nematode
                                          Local Similarity 28.9
mes 13; Conservative
59 CASSQQYQLQTSQCMPACQQSCSQQCQSNTNTQCQPTCQQSCQTS 103
                       Ģ
                    CSQNEYFDSLLHACIP-----CQLRCSSNTPPL---TCQRYCNAS
                                                                                                                                                                             PubMed-9851916;
                                                                                        36605 MW;
                                                     24.78;
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                                                                                                                                                                                                            the EMBL/GenBank/DDBJ databases
                                            7;
                                          Score 59; DB Pred. No. 0.96 7; Mismatches
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ว.96;
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Search completed: Novemi Job time: 14.7983 secs

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